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OM protein - protein search, using sw model

Run on: July 26, 2005, 23:47:55 ; Search time 164 Seconds
(without alignments)

11.791 Million cell updates/sec

Title: US-10-632-678-10

Perfect score: 34

Sequence: 1 CHAVC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	5	2	AAW23979 Cadherin-
2	34	100.0	5	2	AAW91033 Peptide i
3	34	100.0	5	2	AAW91021 Peptide i
4	34	100.0	5	2	AAW17108 Cadherin-
5	34	100.0	5	3	AAW27334 Beta-cate
6	34	100.0	5	3	AAW27346 Beta-cate
7	34	100.0	5	3	AAW73790 N-cadheri
8	34	100.0	5	4	AAW65370 Cyclic pe
9	34	100.0	5	5	AAW47477 Cyclic pe
10	34	100.0	5	6	AAW60211 N-cadheri
11	34	100.0	5	7	AAW43539 Classical
12	34	100.0	5	8	AAW13544 Cadherin-
13	34	100.0	6	4	AAW65445 Cyclic pe
14	34	100.0	6	4	AAW65449 Cyclic pe
15	34	100.0	6	4	AAW65441 Cyclic pe
16	34	100.0	6	4	AAW65444 Cyclic pe
17	34	100.0	6	4	AAW65450 Cyclic pe
18	34	100.0	6	4	AAW65448 Cyclic pe
19	34	100.0	6	5	AAW47551 Peptide,
20	34	100.0	6	5	AAW47521 Cyclic pe
21	34	100.0	6	5	AAW47555 Cyclic pe
22	34	100.0	6	5	AAW47554 Cyclic pe
23	34	100.0	6	5	AAW47558 Cyclic pe
24	34	100.0	6	5	AAW47560 Cyclic pe
25	34	100.0	6	5	AAW47559 Cyclic pe

26	34	100.0	6	7	ABO43613 Classical
27	34	100.0	6	7	ABO43610 Classical
28	34	100.0	6	7	ABO43617 Classical
29	34	100.0	6	7	ABO43618 Classical
30	34	100.0	6	7	ABO43614 Classical
31	34	100.0	6	7	ABO43619 Classical
32	34	100.0	6	8	ADK13619 Cadherin-
33	34	100.0	6	8	ADK13622 Cadherin-
34	34	100.0	6	8	ADK13623 Cadherin-
35	34	100.0	6	8	ADK13615 Cadherin-
36	34	100.0	6	8	ADK13624 Cadherin-
37	34	100.0	6	8	ADK13618 Cadherin-
38	34	100.0	7	4	AAW65447 Cyclic pe
39	34	100.0	7	4	AAW65446 Cyclic pe
40	34	100.0	7	5	AAW47556 Cyclic pe
41	34	100.0	7	5	AAW47563 Cyclic pe
42	34	100.0	7	5	AAW47557 Cyclic pe
43	34	100.0	7	7	ABO43616 Classical
44	34	100.0	7	7	ABO43615 Classical
45	34	100.0	7	8	ADK13620 Cadherin-
46	34	100.0	7	8	ADK13621 Cadherin-
47	34	100.0	8	5	AAW47562 Cyclic pe
48	34	100.0	61	3	AAW68110 Kunitz pr
49	34	100.0	61	3	AAW68085 Kunitz pr
50	34	100.0	121	4	AAU28273 Novel hum
51	34	100.0	198	3	AAW38298 Arabidops
52	34	100.0	198	3	AAW07319 Arabidops
53	34	100.0	244	3	AAW38297 Arabidops
54	34	100.0	244	3	AAW07318 Arabidops
55	34	100.0	380	4	ABW67444 Drosophil
56	34	100.0	381	5	ABW83912 Drosophil
57	34	100.0	537	7	ADW97396 Porcine i
58	34	100.0	542	7	ADW74464 Mycobacte
59	33	97.1	75	8	ADK16783 Nancarcha
60	33	97.1	176	4	AAU50581 Propionib
61	33	97.1	176	6	ABW47100 Propionib
62	33	97.1	428	5	ABW92762 Herbicida
63	33	97.1	672	4	AAW72708 Parvoviru
64	33	97.1	672	4	AAW72710 Parvoviru
65	33	97.1	672	4	AAW72706 Parvoviru
66	33	97.1	672	4	AAW72702 Parvoviru
67	33	97.1	672	4	AAW72704 Parvoviru
68	31	91.2	16	8	ADO34065 Human CLA
69	31	91.2	20	4	AAW15812 Peptide #
70	31	91.2	20	4	ABW34809 Peptide #
71	31	91.2	20	4	AAW28322 Peptide #
72	31	91.2	20	4	ABW29631 Peptide #
73	31	91.2	20	4	ABW20225 Protein #
74	31	91.2	20	4	AAW67996 Human bon
75	31	91.2	20	4	AAW55611 Human bra
76	31	91.2	20	4	ABW49637 Human liv
77	31	91.2	20	4	AAW03550 Peptide #
78	31	91.2	20	5	ABW37528 Human pep
79	31	91.2	53	5	ABW07522 Human ORF
80	31	91.2	58	4	ABW08832 Novel hum
81	31	91.2	61	4	AAW09658 Human pol
82	31	91.2	63	2	AAW27620 Human sec
83	31	91.2	63	4	AAW15142 Peptide #
84	31	91.2	63	4	ABW34134 Peptide #
85	31	91.2	63	4	AAW27597 Peptide #
86	31	91.2	63	4	ABW28966 Peptide #
87	31	91.2	63	4	ABW19575 Protein #
88	31	91.2	63	4	AAW67305 Human bon
89	31	91.2	63	4	AAW54924 Human bra
90	31	91.2	63	4	ABW48967 Human liv
91	31	91.2	63	4	AAW02883 Peptide #
92	31	91.2	63	5	ABW36952 Human pep
93	31	91.2	85	4	AAW24070 Human EST
94	31	91.2	96	4	AAU14419 Human nov
95	31	91.2	96	8	ADW80737 Human pol
96	31	91.2	100	8	ADO34044 Human CLA
97	31	91.2	117	7	ADW05223 Human pro
98	31	91.2	134	4	ABW05990 Novel hum

99 31 91.2 139 7 ADM26297 Adm26297 Hyperther
100 31 91.2 148 6 ABJ18656 Abj18656 Human erb

ALIGNMENTS

RESULT 1
AAW23979
ID AAW23979 standard; peptide; 5 AA.

XX
AC AAW23979;
XX
DT 23-JUL-1998 (first entry)
XX
DE Cadherin-mediated cell adhesion modulating peptide 1.
XX
KW Cadherin-mediated; cell adhesion; drug delivery; treatment; cancer;
KW angiogenesis; skin grafting; neurite growth; veterinary medicine;
KW wound healing; tumour; metastasis; carcinoma; leukaemia; modulation;
KW organ transplant; neurological disease.

XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT Modified-site 5 /note= "optional N-terminal acetylation"
FT Modified-site 5 /note= "optional C-terminal amidation"
XX
XX WO9802452-A2.
XX
XX 22-JAN-1998.
XX
XX 11-JUL-1997; 97WO-CA000489.
XX
XX 12-JUL-1996; 96US-0021612P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ;
XX
XX WPI; 1998-110522/10.

XX
XX Cyclic peptide(s) that modulate cadherin-mediated cell adhesion - used to
PT improve drug delivery through skin, to the brain etc., for treatment of
PT cancer, angiogenesis etc., and to improve grafting of foreign tissue or
PT neurite growth.
XX
XX Claim 8; Page 97; 133pp; English.
XX
XX This is a cyclised peptide capable of modulating cadherin-mediated cell
CC adhesion. Cadherin-expressing cells can be detected from their reaction
CC with the antibody that binds the peptides of the invention. These
CC peptides are useful in human or veterinary medicine to modulate adhesion
CC mediated by E-, N-, P- or R-cadherins (or other cadherins that include
CC the amino acids HAV recognition sequence), specifically where these are
CC expressed by epithelial, endothelial, neural or tumour cells or
CC lymphocytes. The peptides which inhibit cell adhesion are used to improve
CC delivery of drugs through the skin (such that the peptides enters the
CC blood stream), to tumours (particularly ovarian or bladder tumours or
CC melanoma) and to the brain. They are also used to treat cancer
CC (carcinoma, leukaemia or melanoma), inhibit metastasis and also inhibit
CC angiogenesis. The peptides that stimulate adhesion are used to improve
CC wound healing to promote adherence of foreign tissues (skin grafts or
CC organ transplants), and to improve adherence to tissue culture surfaces
CC and bio-reactors. Other uses of the peptides are to induce apoptosis in
CC cadherin-expressing cells, increase or decrease neurite outgrowth, to
CC treat spinal cord injuries and de-myelinating neurological diseases
CC (specifically multiple sclerosis). They can be used for modulating the
CC immune system (e.g. in cases of diabetes or rheumatoid arthritis), for
CC preventing pregnancy and to increase vaso-permeability. The antibodies
CC which bind to these peptides are also used to modulate cell adhesion and

CC when coupled to a drug, to target the drug to cadherin-expressing cells.
CC Diagnostic agents may also be delivered using the peptides in a skin
CC patch, particularly where the agent generates a colour in contact with,
CC e.g. cocaine, human immunodeficiency viral proteins, glucose or prostate-
CC specific antigen, particularly for home-testing kits. The peptides make
CC it possible to deliver a wide range of drugs through the skin, avoiding
CC parental administration, by-passing the gastro- intestinal system and
CC improving patient compliance
XX
XX Sequence 5 AA;

Query Match 100.0%; Score 34; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1 CHAVC 5

RESULT 2
AAW91033
ID AAW91033 standard; peptide; 5 AA.

XX
AC AAW91033;
XX
DT 24-MAR-1999 (first entry)
XX
DE Peptide inhibiting interaction of alpha-catenin and beta-catenin.
XX
KW Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion;
KW cadherin-mediated function; demyelinating neurological disease;
KW multiple sclerosis; drug delivery; cancer; angiogenesis; immune system;
KW central nervous system; apoptosis induction; cadherin-expression cell;
KW pregnancy prevention; vasopermeability; synaptic stability; diabetes;
KW rheumatoid arthritis; allergic response; learning; memory;
KW antibody-mediated graft rejection; cyclic.

OS Synthetic.
XX
XX WO9845319-A2.
XX
XX 15-OCT-1998.
XX
XX 14-APR-1998; 98WO-CA000322.
XX
XX 10-APR-1997; 97US-0043361P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ;
XX
XX WPI; 1999-024009/02.

XX
XX New catenin modulating agents - comprising peptides having a sequence HAV
PT or analogues or antibodies, used for modulating cadherin-mediated
PT functions.
XX
XX Claim 12; Page 78; 106pp; English.
XX
XX The present sequence represents a peptide which is capable of inhibiting
CC an interaction between alpha-catenin and beta-catenin. The peptide is
CC used in modulating agents that are used for modulating cadherin-mediated
CC functions. They can be used for disrupting interaction between alpha-
CC catenin and beta-catenin in a cell, inhibiting cell adhesion, e.g.
CC between epithelial cells, endothelial cells, neural cells, tumour cells
CC and lymphocytes, for treating a demyelinating neurological disease, e.g.
CC multiple sclerosis, for reducing unwanted cellular adhesion in a mammal,
CC for enhancing the delivery of a drug through the skin of a mammal, for
CC enhancing the delivery of a drug to a tumour in a mammal, for treating
CC cancer in a mammal, for inhibiting angiogenesis in a mammal, for
CC enhancing drug delivery to the central nervous system of a mammal, for
CC inducing apoptosis in a cadherin-expression cell, for modulating the

CC immune system of a mammal, for preventing pregnancy in a mammal, for
 CC increasing vasopermeability in a mammal, or for inhibiting synaptic
 CC stability in a mammal. In particular they can be used for treating
 CC diabetes, rheumatoid arthritis, allergic responses, antibody-mediated
 CC graft rejection or for stimulating learning and memory
 XX
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 34; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 1 CHAVC 5
 RESULT 3
 AAW91021
 ID AAW91021 standard; peptide; 5 AA.
 AC AAW91021;
 XX
 XX 24-MAR-1999 (first entry)
 DT
 XX
 XX Peptide inhibiting interaction of alpha-catenin and beta-catenin.
 DE
 XX Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion;
 KW cadherin-mediated function; demyelinating neurological disease;
 KW multiple sclerosis; drug delivery; cancer; angiogenesis; immune system;
 KW central nervous system; apoptosis induction; cadherin-expression cell;
 KW pregnancy prevention; vasopermeability; synaptic stability; diabetes;
 KW rheumatoid arthritis; allergic response; learning; memory;
 KW antibody-mediated graft rejection.
 XX
 OS Synthetic.
 XX
 XX WO9845319-A2.
 PN
 XX 15-OCT-1998.
 PD
 XX 14-APR-1998; 98WO-CA000322.
 PF
 XX 10-APR-1997; 97US-00433361P.
 PR
 XX (UYMC-) UNIV MCGILL.
 PA
 XX Blaschuk OW, Gour BJ;
 PI WPI; 1999-024009/02.
 XX
 XX New catenin modulating agents - comprising peptides having a sequence HAV
 PT or analogues or antibodies, used for modulating cadherin-mediated
 PT functions.
 XX
 XX Claim 10; Page 77; 106pp; English.
 PS
 XX The present sequence represents a peptide which is capable of inhibiting
 CC an interaction between alpha-catenin and beta-catenin. The peptide is
 CC used in modulating agents that are used for modulating cadherin-mediated
 CC functions. They can be used for disrupting interaction between alpha-
 CC catenin and beta-catenin in a cell, inhibiting cell adhesion, e.g.
 CC between epithelial cells, endothelial cells, neural cells, tumour cells
 CC and lymphocytes, for treating a demyelinating neurological disease, e.g.
 CC multiple sclerosis, for reducing unwanted cellular adhesion in a mammal,
 CC for enhancing the delivery of a drug through the skin of a mammal, for
 CC enhancing the delivery of a drug to a tumour in a mammal, for treating
 CC cancer in a mammal, for inhibiting angiogenesis in a mammal, for
 CC enhancing drug delivery to the central nervous system of a mammal, for
 CC inducing apoptosis in a cadherin-expression cell, for modulating the
 CC immune system of a mammal, for preventing pregnancy in a mammal, for
 CC increasing vasopermeability in a mammal, or for inhibiting synaptic
 CC stability in a mammal. In particular they can be used for treating

CC diabetes, rheumatoid arthritis, allergic responses, antibody-mediated
 CC graft rejection or for stimulating learning and memory
 XX
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 34; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 1 CHAVC 5
 RESULT 4
 AAY17108
 ID AAY17108 standard; peptide; 5 AA.
 XX
 AC AAY17108;
 XX
 XX 20-SEP-1999 (first entry)
 DT
 XX
 XX Cadherin-mediated adhesion modulating cyclic peptide.
 DE
 XX Cell adhesion modulation; CAM; synaptic stability; cadherin;
 KW cadherin-mediated adhesion; drug delivery; cell adhesion; tumour;
 KW wound healing; neurite outgrowth; cyclic; circular.
 KW
 XX Synthetic.
 OS
 XX WO9933875-A1.
 PN
 XX 08-JUL-1999.
 PD
 XX 23-DEC-1998; 98WO-CA001207.
 PF
 XX 23-DEC-1997; 97US-00996679.
 PR
 XX (UYMC-) UNIV MCGILL.
 PA
 XX Blaschuk OW, Gour BJ;
 PI WPI; 1999-430231/36.
 XX
 XX Cyclic peptide cell adhesion modulating agents, useful for modulating
 PT synaptic stability.
 PT
 XX Claim 8; Page 64; 144pp; English.
 PS
 XX The invention provides cyclic peptide cell adhesion modulating (CAM)
 CC agents that comprises a His-Ala-Val recognition sequence. Also provided
 CC is a method for inhibiting synaptic stability in a mammal that comprises
 CC administering to a mammal a therapeutically effective amount of a CAM
 CC agent that inhibits cadherin-mediated adhesion, where the agent comprises
 CC a cyclic peptide having a peptide ring, and where the sequence His-Ala-
 CC Val is present within the peptide ring. The cyclic peptides are cell
 CC adhesion modulating agents that inhibit cadherin-mediated adhesion. They
 CC can be used in a method for inhibiting synaptic stability in mammals. The
 CC agents can be used to treat diseases or other conditions characterized by
 CC undesirable cell adhesion or to facilitate drug delivery to a specific
 CC tissue or tumour. Alternatively the agents may be used to enhance cell
 CC adhesion (e.g. to supplement or replace stitches or to facilitate wound
 CC healing) or to enhance or direct neurite outgrowth
 XX
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 34; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 1 CHAVC 5

OS Homo sapiens.
 XX
 FN WO9557565-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000362.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuck OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-062165/05.
 XX
 XX Detecting expression of OB-cadherin or N-cadherin used for diagnosing and
 FT evaluating cancer.
 PT
 PS Disclosure; Page 21; 56pp; English.
 XX
 CC The present invention describes methods which have been developed for
 CC detecting and evaluating cancer that are based on the finding that OB-
 CC cadherin and N-cadherin are expressed by metastatic carcinoma cells, but
 CC not by highly differentiated, poorly invasive carcinomas. A method for
 CC determining the presence or absence of a cancer in a patient comprises:
 CC (1) contacting a biological sample from the patient with a binding agent
 CC that specifically binds to OB- or N-cadherin OR with an oligonucleotide
 CC that hybridizes to a polynucleotide that encodes OB- or N-cadherin; and
 CC (2) detecting in the sample an amount of polypeptide that binds to the
 CC binding agent OR the amount of polynucleotide that hybridizes to the
 CC oligonucleotide, relative to a predetermined cut-off value, and
 CC determining the presence or absence of cancer in the patient from this.
 CC The methods from the present invention can be used to determine the
 CC metastatic potential of a cancer. The methods may be used to detect a
 CC metastatic cancer in a patient, to monitor progression of a cancer, or to
 CC evaluate the metastatic potential of a cancer. Cancers which may be
 CC evaluated using the methods include leukemia, prostate cancer, breast
 CC cancer and ovarian cancer. AAY73501 to AAY73813 represent peptide
 CC sequences used in the exemplification of the present invention.
 CC Specifically, AAY73503 to AAY73789 represent OB-cadherin cell adhesion
 CC recognition (CAR) peptides and AAY73790 to AAY73808 represent N-cadherin
 CC CAR peptides. AAY73906 to AAY73915 represent PCR primers used in examples
 CC from the present invention
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 34; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 Db 1 CHAVC 5
 RESULT 8
 AAG65370
 ID AAG65370 standard; peptide; 5 AA.
 XX
 AC AAG65370;
 XX
 XX 30-NOV-2001 (first entry)
 DT
 DE Cyclic peptide with classical cadherin CAR sequence.
 XX
 XX Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR;
 KW cytosolic; vulnarary; immunomodulator; vasotropic; neuroprotective;
 KW cerebroprotective; muscular; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetylation"
 FT Modified-site 5
 FT /note= "C-terminal amide"
 XX
 FN WO200153331-A2.
 XX
 XX 26-JUL-2001.
 PD
 XX 24-JAN-2001; 2001WO-US002508.
 PF
 XX 24-JAN-2000; 2000US-00491078.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;
 XX
 DR WPI; 2001-549899/61.
 XX
 XX Cell adhesion modulating agent used for enhancing delivery of drug to
 FT tumor comprises imidazole compounds.
 PT
 PS Claim 15; Page 146; 436pp; English.
 XX
 CC The invention relates to cell adhesion modulating agents that comprise
 CC imidazole compounds of specified formulae that are peptidomimetics of
 CC cyclic peptides. The peptidomimetics have a structure similar to that of
 CC a cyclic peptide that comprises a cadherin cell recognition sequence HAV.
 CC The agents are used for modulating classical cadherin mediated
 CC intercellular adhesion, reducing unwanted cellular adhesion, enhancing
 CC delivery of a drug to a tumor, inhibiting development of cancer,
 CC inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing
 CC wound healing, modulating the immune system, increasing vasopermeability,
 CC treating demyelinating disease, facilitating migration of an N-cadherin
 CC expressing cell on astrocytes, inhibiting synaptic stability, modulating
 CC neurite outgrowth, and treating spinal cord injuries and macular
 CC degeneration. The present sequence represents a cyclic peptide with
 CC classical cadherin cell adhesion recognition (CAR) sequence
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 34; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 Db 1 CHAVC 5
 RESULT 9
 AAM47477
 ID AAM47477 standard; peptide; 5 AA.
 XX
 AC AAM47477;
 XX
 XX 12-FEB-2002 (first entry)
 DT
 DE Cyclic peptide endothelial cell adhesion modulator #1.
 XX
 XX Cadherin; cytosolic; gynecological; endometriosis;
 KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
 KW cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Linked to residue 5 to form a cyclic peptide, N-
 FT terminal acetyl or N-terminal CH3-SO2 group"

FT Modified-site 5 /note= "Linked to residue 1 to form a cyclic peptide, C-terminal amide"
FT XX
FT XX
PN WO200177146-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 09-APR-2001; 2001WO-US011669.
PF
XX
XX 07-APR-2000; 2000US-00544782.
PR
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
PI WPI; 2002-049129/06.
XX
XX
XX Modulating endothelial cell adhesion for inhibiting development of
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting
PT cell with a cyclic peptide having cadherin cell adhesion recognition
PT sequence.
XX
XX Claim 6; Page 64; 139pp; English.
PS
XX The present invention relates to a method for modulating endothelial cell
CC adhesion. The method comprises contacting an endothelial cell with a
CC modulating peptide comprising a cadherin cell adhesion recognition
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful
CC for inhibiting angiogenesis, increasing vasopermeability, increasing
CC blood flow to a tumour, disrupting neovasculation and inhibiting the
CC development of endometriosis in a mammal. The modulating peptide reduces
CC unwanted endothelial adhesion occurring between tumour cells, tumour
CC cells and normal cells, normal cells as a result of surgery, injury,
CC chemotherapy, disease and inflammation. The present sequence is one such
CC modulating peptide
XX
XX Sequence 5 AA;
SQ

Query Match 100.0%; Score 34; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db |||||
1 CHAVC 5

RESULT 10
ABU60211
ID ABU60211 standard; peptide; 5 AA.
XX
XX ABU60211;
AC
XX
XX 24-APR-2003 (first entry)
DT
DE N-cadherin cell adhesion recognition sequence #1.
XX
XX Metastasis; cancer; binding agent; cell adhesion recognition; CAR;
KW OB-cadherin; N-cadherin; prostate cancer; ovarian cancer; breast cancer;
KW leukaemia.
XX
XX Synthetic.
OS
XX US2002146687-A1.
PN
XX 10-OCT-2002.
PD
XX 05-MAY-1999; 99US-00305928.
PF
XX 05-MAY-1998; 98US-00073040.
PR
XX 06-NOV-1998; 98US-00187859.
PR
XX 20-JAN-1999; 99US-00234395.
PR

XX (BLAS/) BLASCHUK O W.
PA (SYMO/) SYMONDS J M.
PA (BYER/) BYERS S.
PA (GOUR/) GOUR B J.
XX
XX Blaschuk OW, Symonds JM, Byers S, Gour BJ;
PI WPI; 2003-255125/25.
DR
XX
XX Diagnosing or evaluating metastatic potential of cancer in patient by
PT contacting biological sample obtained from patient with specified binding
PT agent or oligonucleotide, and detecting polypeptide that binds to the
PT binding agent.
XX
XX Disclosure; Page 8; 94pp; English.
PS
XX The invention discloses a method for diagnosing or evaluating metastatic
CC potential of cancer in a patient. The method comprises contacting a
CC biological sample obtained from the patient with a binding agent,
CC preferentially antibodies or cell adhesion recognition (CAR) sequences,
CC that specifically bind to OB-cadherin or N-cadherin or an oligonucleotide
CC that hybridises to a polynucleotide encoding OB-cadherin or N-cadherin
CC and then detecting the amount of polypeptide that binds to the binding
CC agent. The inventive method is useful for diagnosing or evaluating
CC metastatic potential of cancer, such as prostate, ovarian or breast
CC cancer, as well as leukaemia in a patient. It can also be employed for
CC monitoring the progression of cancer in a patient. The inventive method
CC provides accurate diagnosis or evaluation of metastatic potential of
CC cancer in a patient in a simple and economical manner. The sequences
CC presented in ABUS9926-ABUS9969 and ABU60211-ABU60229 are OB-cadherin or N
CC -cadherin, respectively, CAR sequences
XX
XX Sequence 5 AA;
SQ

Query Match 100.0%; Score 34; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db |||||
1 CHAVC 5

RESULT 11
ABO43539
ID ABO43539 standard; peptide; 5 AA.
XX
XX ABO43539;
AC
XX 25-SEP-2003 (first entry)
DT
DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #1.
XX
XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
KW central nervous system; wound healing; vasopermeability; N-cadherin;
KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;
KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;
KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
KW cell adhesion recognition sequence.
XX
XX Synthetic.
OS
XX US2002168761-A1.
PN
XX 14-NOV-2002.
PD
XX 24-JAN-2001; 2001US-00769145.
PF
XX 24-JAN-2000; 2000US-00491078.
PR
XX

PA (GOUR/) GOUR B J.
 PA (BLAS/) BLASCHUK O W.
 PA (ALIA/) ALI A.
 PA (NIFF/) NI F.
 PA (CHEN/) CHEN Z.
 PA (MICH/) MICHAUD S D.
 PA (WANG/) WANG S.
 PA (HUZZ/) HU Z.
 XX GOUR BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;
 XX WPI; 2003-521524/49.
 XX
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated
 PT intercellular adhesion, for enhancing wound healing, has three-
 PT dimensional structure similar to three-dimensional structure of cyclic
 PT peptide.
 XX
 XX Claim 15; Page 99; 309pp; English.
 XX
 XX The invention relates to a cell adhesion modulating agent which is a
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent
 CC is useful for modulating classical cadherin-mediated intercellular
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for
 CC enhancing the delivery of a drug to a tumour, for inhibiting the
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug
 CC delivery to the central nervous system, for enhancing wound healing, for
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for
 CC modulating the immune system of a mammal, for increasing
 CC vasopermeability, for treating a demyelinating neurological disease, for
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for
 CC treating spinal cord injuries and for treating macular degeneration. The
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell
 CC leukaemia, excessive immune reactions involving the humoral immune system
 CC and generation of immunoglobulins and diseases associated with excessive
 CC generation of T cells. This sequence represents a cadherin (CAD) cell
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
 CC invention
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 34; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 1 CHAVC 5
 RESULT 12
 ADK13544
 ID ADK13544 standard; peptide; 5 AA.
 XX
 AC ADK13544;
 XX
 XX 17-JUN-2004 (first entry)
 DT
 XX
 XX Cadherin-mediated cell adhesion-modulating peptidomimetic #3.
 DE
 XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
 KW angiogenesis; central nervous system; wound healing;
 KW foreign tissue adhesion; vasopermeability;
 KW demyelinating neurological disease; astrocyte; synaptic stability;
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.

XX Synthetic.
 OS US2004058864-A1.
 PN 25-MAR-2004.
 PD
 XX 10-APR-2003; 2003US-00412701.
 XX 24-JAN-2000; 2000US-00491078.
 PR 24-JAN-2001; 2001US-00769145.
 PR
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA
 XX GOUR BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;
 XX WPI; 2004-268836/25.
 DR
 XX New cell adhesion modulating agent, useful for treating or preventing
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing
 PT wound healing, treating a demyelinating neurological disease or treating
 PT spinal cord injuries.
 PT
 XX Claim 15; SEQ ID NO 10; 281pp; English.
 PS
 XX The invention relates to a cell adhesion-modulating agent. The invention
 CC also relates to methods for screening a candidate compound for the
 CC ability to modulate classical cadherin-mediated cell adhesion,
 CC identifying a compound that modulates classical cadherin-mediated cell
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
 CC to the central nervous system of a mammal, enhancing wound healing in a
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,
 CC modulating the immune system of a mammal, increasing vasopermeability in
 CC a mammal, treating a demyelinating neurological disease in a mammal,
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,
 CC treating spinal cord injuries in a mammal, and treating macular
 CC degeneration in a mammal. The compounds are useful for inhibiting or
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating
 CC agents are useful for inhibiting the development of cancer, e.g. treating
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The
 CC agents are also useful in inhibiting angiogenesis, for enhancing the
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in
 CC to the central nervous system of a mammal, for enhancing drug delivery
 CC a mammal, for enhancing the adhesion of foreign tissue implanted within a
 CC mammal, for modulating the immune system of a mammal, for treating a
 CC demyelinating neurological disease (such as multiple sclerosis) in a
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for
 CC treating macular degeneration in a mammal. This sequence represents a
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a
 CC classical cadherin cell adhesion recognition (CAR) sequence.
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 34; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 1 CHAVC 5
 RESULT 13
 AAG65445
 ID AAG65445 standard; peptide; 6 AA.
 XX

[illegible]


```
PR 07-APR-2000; 2000US-00544782.
XX (UYMC-) UNIV MCGILL.
PA Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Claim 1; Page 49; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing the
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence was used to
XX illustrate the present invention
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 34; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAUC 5
Db 1 CHAUC 5
RESULT '20
AAM47521
ID AAM47521 standard; peptide; 6 AA.
XX
XX AC AAM47521;
XX
XX DT 12-FEB-2002 (first entry)
XX
XX DE Cyclic peptide endothelial cell adhesion modulator #14.
XX
XX KW Cadherin; cytostatic; gynecological; endometriosis;
XX endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
XX cyclic.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "Linked to residue 6 to form a cyclic peptide, N-
XX terminal acetyl or N-terminal CH3-SO2 group"
XX
XX Modified-site 6
XX /note= "Linked to residue 1 to form a cyclic peptide, C-
XX terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX
XX (UYMC-) UNIV MCGILL.
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
PI
```

```
XX WPI; 2002-049129/06.
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Claim 6; Page 64; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing the
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence is one such
XX modulating peptide
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 34; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAUC 5
Db 2 CHAUC 6
RESULT 21
AAM47555
ID AAM47555 standard; peptide; 6 AA.
XX
XX AC AAM47555;
XX
XX DT 12-FEB-2002 (first entry)
XX
XX DE Cyclic peptide endothelial cell adhesion modulator #37.
XX
XX KW Cadherin; cytostatic; gynecological; endometriosis;
XX endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
XX cyclic.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "Linked to residue 6 to form a cyclic peptide, N-
XX terminal acetyl"
XX
XX Modified-site 6
XX /note= "Linked to residue 1 to form a cyclic peptide, C-
XX terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX
XX (UYMC-) UNIV MCGILL.
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
```


CC blood flow to a tumour, disrupting neovasculature and inhibiting the
CC development of endometriosis in a mammal. The modulating peptide reduces
CC unwanted endothelial adhesion occurring between tumour cells, tumour
CC cells and normal cells, normal cells as a result of surgery, injury,
CC chemotherapy, disease and inflammation. The present sequence is one such
CC modulating peptide
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1 CHAVC 5

RESULT 24
AAM47560
ID AAM47560 standard; peptide; 6 AA.

AC AAM47560;

XX 12-FEB-2002 (first entry)

DE Cyclic peptide endothelial cell adhesion modulator #21.

XX Cadherin; cytostatic; gynecological; endometriosis;
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
KW cyclic.
XX Synthetic.

OS
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Linked to residue 6 to form a cyclic peptide, N-
FT terminal acetyl or N-terminal CH3-SO2 group"
FT Modified-site 6
FT /note= "Linked to residue 1 to form a cyclic peptide, C-
FT terminal amide"

WO200177146-A2.
18-OCT-2001.

XX 09-APR-2001; 2001WO-US011669.

XX 07-APR-2000; 2000US-00544782.

XX (UYMC-) UNIV MCGILL.

XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;

XX WPI; 2002-049129/06.

XX Modulating endothelial cell adhesion for inhibiting development of
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting
PT cell with a cyclic peptide having cadherin cell adhesion recognition
PT sequence.

XX Claim 6; Page 64; 139pp; English.

XX The present invention relates to a method for modulating endothelial cell
CC adhesion. The method comprises contacting an endothelial cell with a
CC modulating peptide comprising a cadherin cell adhesion recognition
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful
CC for inhibiting angiogenesis, increasing vasopermeability, increasing
CC blood flow to a tumour, disrupting neovasculature and inhibiting the
CC development of endometriosis in a mammal. The modulating peptide reduces
CC unwanted endothelial adhesion occurring between tumour cells, tumour
CC cells and normal cells, normal cells as a result of surgery, injury,
CC chemotherapy, disease and inflammation. The present sequence is one such

CC modulating peptide
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1 CHAVC 5

RESULT 25
AAM47559
ID AAM47559 standard; peptide; 6 AA.

AC AAM47559;

XX 12-FEB-2002 (first entry)

DE Cyclic peptide endothelial cell adhesion modulator #20.

XX Cadherin; cytostatic; gynecological; endometriosis;
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
KW cyclic.
XX Synthetic.

OS
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Linked to residue 6 to form a cyclic peptide, N-
FT terminal acetyl or N-terminal CH3-SO2 group"
FT Modified-site 6
FT /note= "Linked to residue 1 to form a cyclic peptide, C-
FT terminal amide"

WO200177146-A2.

18-OCT-2001.

XX 09-APR-2001; 2001WO-US011669.

XX 07-APR-2000; 2000US-00544782.

XX (UYMC-) UNIV MCGILL.

XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;

XX WPI; 2002-049129/06.

XX Modulating endothelial cell adhesion for inhibiting development of
PT endometriosis, increasing blood flow to tumor in a mammal, by contacting
PT cell with a cyclic peptide having cadherin cell adhesion recognition
PT sequence.

XX Claim 6; Page 64; 139pp; English.

XX The present invention relates to a method for modulating endothelial cell
CC adhesion. The method comprises contacting an endothelial cell with a
CC modulating peptide comprising a cadherin cell adhesion recognition
CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful
CC for inhibiting angiogenesis, increasing vasopermeability, increasing
CC blood flow to a tumour, disrupting neovasculature and inhibiting the
CC development of endometriosis in a mammal. The modulating peptide reduces
CC unwanted endothelial adhesion occurring between tumour cells, tumour
CC cells and normal cells, normal cells as a result of surgery, injury,
CC chemotherapy, disease and inflammation. The present sequence is one such
CC modulating peptide

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db |||||
1 CHAVC 5

Sequence 6 AA;
Query Match 100.0%; Score 34; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db |||||
1 CHAVC 5

RESULT 26
ABO43613
ID ABO43613 standard; peptide; 6 AA.
XX
AC ABO43613;
XX
DT 25-SEP-2003 (first entry)
XX
DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #73.
XX
KW Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
KW central nervous system; wound healing; vasopermeability; N-cadherin;
KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;
KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;
KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
KW cell adhesion recognition sequence.
XX
OS Synthetic.
XX
PN US2002168761-A1.
XX
PD 14-NOV-2002.
XX
PF 24-JAN-2001; 2001US-00769145.
XX
PR 24-JAN-2000; 2000US-00491078.
XX
PA (GOUR/) GOUR B J.
PA (BLAS/) BLASCHUK O W.
PA (ALIA/) ALI A.
PA (NIFE/) NI F.
PA (CHEN/) CHEN Z.
PA (MICH/) MICHAUD S D.
PA (WANG/) WANG S.
PA (HUZZ/) HU Z.
XX
PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
PI Hu Z;
XX
DR WPI; 2003-521524/49.
XX
PT Novel cell adhesion modulating agent for modulating cadherin-mediated
PT intercellular adhesion, for enhancing wound healing, has three-
PT dimensional structure similar to three-dimensional structure of cyclic
PT peptide.
XX
PS Disclosure; Page 7; 309pp; English.
XX
CC The invention relates to a cell adhesion modulating agent which is a
CC peptidomimetic having a three-dimensional structure of a cyclic peptide
CC that comprises the sequence HAV within a cyclic peptide ring. The agent
CC is useful for modulating classical cadherin-mediated intercellular
CC adhesion, for reducing unwanted cellular adhesion in a mammal, for
CC enhancing the delivery of a drug to a tumour, for inhibiting the
CC development of cancer, for inhibiting angiogenesis, for enhancing drug
CC delivery to the central nervous system, for enhancing wound healing, for
CC enhancing the adhesion of foreign tissue implanted within a mammal, for
CC modulating the immune system of a mammal, for increasing
CC vasopermeability, for treating a demyelinating neurological disease, for
CC facilitating migration of an N-cadherin expressing cell on astrocytes,
CC for inhibiting synaptic stability, for modulating neurite outgrowth, for
CC treating spinal cord injuries and for treating macular degeneration. The
CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or

CC leukaemia. The agent is useful for treating skin disorders, acute B cell
CC leukaemia, excessive immune reactions involving the humoral immune system
CC and generation of immunoglobulins and diseases associated with excessive
CC generation of T cells. This sequence represents a cadherin (CAD) cell
CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
CC invention
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db |||||
1 CHAVC 5

RESULT 27
ABO43610
ID ABO43610 standard; peptide; 6 AA.
XX
AC ABO43610;
XX
DT 25-SEP-2003 (first entry)
XX
DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #70.
XX
KW Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
KW central nervous system; wound healing; vasopermeability; N-cadherin;
KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;
KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;
KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
KW cell adhesion recognition sequence.
XX
OS Synthetic.
XX
PN US2002168761-A1.
XX
PD 14-NOV-2002.
XX
PF 24-JAN-2001; 2001US-00769145.
XX
PR 24-JAN-2000; 2000US-00491078.
XX
PA (GOUR/) GOUR B J.
PA (BLAS/) BLASCHUK O W.
PA (ALIA/) ALI A.
PA (NIFE/) NI F.
PA (CHEN/) CHEN Z.
PA (MICH/) MICHAUD S D.
PA (WANG/) WANG S.
PA (HUZZ/) HU Z.
XX
PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
PI Hu Z;
XX
DR WPI; 2003-521524/49.
XX
PT Novel cell adhesion modulating agent for modulating cadherin-mediated
PT intercellular adhesion, for enhancing wound healing, has three-
PT dimensional structure similar to three-dimensional structure of cyclic
PT peptide.
XX
PS Claim 15; Page 99; 309pp; English.
XX
CC The invention relates to a cell adhesion modulating agent which is a
CC peptidomimetic having a three-dimensional structure of a cyclic peptide
CC that comprises the sequence HAV within a cyclic peptide ring. The agent
CC is useful for modulating classical cadherin-mediated intercellular
CC adhesion, for reducing unwanted cellular adhesion in a mammal, for

enhancing the delivery of a drug to a tumour, for inhibiting the development of cancer, for inhibiting angiogenesis, for enhancing drug delivery to the central nervous system, for enhancing wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for increasing vasopermeability, for treating a demyelinating neurological disease, for facilitating migration of an N-cadherin expressing cell on astrocytes, for inhibiting synaptic stability, for modulating neurite outgrowth, for treating spinal cord injuries and for treating macular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agent is useful for treating skin disorders, acute B cell leukaemia, excessive immune reactions involving the humoral immune system and generation of immunoglobulins and diseases associated with excessive generation of T cells. This sequence represents a cadherin (CAD) cell adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the invention

Sequence 6 AA;

Query Match 100.0%; Score 34; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
| | | | |
Db 1 CHAVC 5

RESULT 28
ABO43617
ID ABO43617 standard; peptide; 6 AA.
XX
AC ABO43617;
XX
DT 25-SEP-2003 (first entry)
XX
DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #77.
XX
KW Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
KW central nervous system; wound healing; vasopermeability; N-cadherin;
KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;
KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;
KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
KW cell adhesion recognition sequence.
XX
OS Synthetic.
XX
PN US2002168761-A1.
XX
PD 14-NOV-2002.
XX
PF 24-JAN-2001; 2001US-00769145.
XX
PR 24-JAN-2000; 2000US-00491078.
XX
PA (GOUR/) GOUR B J.
PA (BLAS/) BLASCHUK O W.
PA (ALIA/) ALI A.
PA (NIFF/) NI F.
PA (CHEN/) CHEN Z.
PA (MICH/) MICHAUD S D.
PA (WANG/) WANG S.
PA (HUZZ/) HU Z.
XX
PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
PI Hu Z;
XX
XX WPI; 2003-521524/49.
XX
PT Novel cell adhesion modulating agent for modulating cadherin-mediated intercellular adhesion, for enhancing wound healing, has three-

dimensional structure similar to three-dimensional structure of cyclic peptide.

Disclosure; Page 7; 309pp; English.

The invention relates to a cell adhesion modulating agent which is a peptidomimetic having a three-dimensional structure of a cyclic peptide that comprises the sequence HAV within a cyclic peptide ring. The agent is useful for modulating classical cadherin-mediated intercellular adhesion, for reducing unwanted cellular adhesion in a mammal, for enhancing the delivery of a drug to a tumour, for inhibiting the development of cancer, for inhibiting angiogenesis, for enhancing drug delivery to the central nervous system, for enhancing wound healing, for enhancing the adhesion of foreign tissue implanted within a mammal, for modulating the immune system of a mammal, for increasing vasopermeability, for treating a demyelinating neurological disease, for facilitating migration of an N-cadherin expressing cell on astrocytes, for inhibiting synaptic stability, for modulating neurite outgrowth, for treating spinal cord injuries and for treating macular degeneration. The cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The agent is useful for treating skin disorders, acute B cell leukaemia, excessive immune reactions involving the humoral immune system and generation of immunoglobulins and diseases associated with excessive generation of T cells. This sequence represents a cadherin (CAD) cell adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the invention

Sequence 6 AA;

Query Match 100.0%; Score 34; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
| | | | |
Db 1 CHAVC 5

RESULT 29
ABO43618
ID ABO43618 standard; peptide; 6 AA.
XX
AC ABO43618;
XX
DT 25-SEP-2003 (first entry)
XX
DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #78.
XX
KW Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
KW central nervous system; wound healing; vasopermeability; N-cadherin;
KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;
KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;
KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
KW cell adhesion recognition sequence.
XX
OS Synthetic.
XX
PN US2002168761-A1.
XX
PD 14-NOV-2002.
XX
PF 24-JAN-2001; 2001US-00769145.
XX
PR 24-JAN-2000; 2000US-00491078.
XX
PA (GOUR/) GOUR B J.
PA (BLAS/) BLASCHUK O W.
PA (ALIA/) ALI A.
PA (NIFF/) NI F.
PA (CHEN/) CHEN Z.
PA (MICH/) MICHAUD S D.

PA (WANG/) WANG S.
 PA (HUZZ/) HU Z.
 XX
 XX
 PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;
 XX
 XX WPI; 2003-521524/49.
 DR
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated
 PT intercellular adhesion, for enhancing wound healing, has three-
 PT dimensional structure similar to three-dimensional structure of cyclic
 PT peptide.
 XX
 XX Disclosure; Page 7; 309pp; English.
 PS
 XX The invention relates to a cell adhesion modulating agent which is a
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent
 CC is useful for modulating classical cadherin-mediated intercellular
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for
 CC enhancing the delivery of a drug to a tumour, for inhibiting the
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug
 CC delivery to the central nervous system, for enhancing wound healing, for
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for
 CC modulating the immune system of a mammal, for increasing
 CC vasopermeability, for treating a demyelinating neurological disease, for
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for
 CC treating spinal cord injuries and for treating macular degeneration. The
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell
 CC leukaemia, excessive immune reactions involving the humoral immune system
 CC and generation of immunoglobulins and diseases associated with excessive
 CC generation of T cells. This sequence represents a cadherin (CAD) cell
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
 CC invention
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 34; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 |||||
 Db 1 CHAVC 5
 RESULT 30
 ABO43614
 ID ABO43614 standard; peptide; 6 AA.
 XX
 AC ABO43614;
 XX
 DT 25-SEP-2003 (first entry)
 XX
 DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #74.
 XX
 XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
 KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
 KW central nervous system; wound healing; vasopermeability; N-cadherin;
 KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;
 KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;
 KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
 KW cell adhesion recognition sequence.
 XX
 XX Synthetic.
 OS
 XX US2002168761-A1.
 PN
 XX 14-NOV-2002.
 PD
 XX

PF 24-JAN-2001; 2001US-00769145.
 XX
 PR 24-JAN-2000; 2000US-00491078.
 XX
 XX (GOUR/) GOUR B J.
 PA (BLAS/) BLASCHUK O W.
 PA (ALIA/) ALI A.
 PA (NIEF/) NI F.
 PA (CHEN/) CHEN Z.
 PA (MICH/) MICHAUD S D.
 PA (WANG/) WANG S.
 PA (HUZZ/) HU Z.
 XX
 PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;
 XX
 XX WPI; 2003-521524/49.
 XX
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated
 PT intercellular adhesion, for enhancing wound healing, has three-
 PT dimensional structure similar to three-dimensional structure of cyclic
 PT peptide.
 XX
 PS Disclosure; Page 7; 309pp; English.
 XX
 CC The invention relates to a cell adhesion modulating agent which is a
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent
 CC is useful for modulating classical cadherin-mediated intercellular
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for
 CC enhancing the delivery of a drug to a tumour, for inhibiting the
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug
 CC delivery to the central nervous system, for enhancing wound healing, for
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for
 CC modulating the immune system of a mammal, for increasing
 CC vasopermeability, for treating a demyelinating neurological disease, for
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for
 CC treating spinal cord injuries and for treating macular degeneration. The
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell
 CC leukaemia, excessive immune reactions involving the humoral immune system
 CC and generation of immunoglobulins and diseases associated with excessive
 CC generation of T cells. This sequence represents a cadherin (CAD) cell
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
 CC invention
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 34; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 |||||
 Db 2 CHAVC 6
 RESULT 31
 ABO43619
 ID ABO43619 standard; peptide; 6 AA.
 XX
 AC ABO43619;
 XX
 DT 25-SEP-2003 (first entry)
 XX
 DE Classical cadherin CAR sequence cyclic peptide peptidomimetic #79.
 XX
 XX Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;
 KW cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;
 KW central nervous system; wound healing; vasopermeability; N-cadherin;
 KW demyelinating neurological disease; astrocyte; synaptic stability; ovary;
 KW neurite outgrowth; spinal cord injury; macular degeneration; bladder;
 KW

KW melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;
 KW immune reaction; immunoglobulin; T cell generation; CAR; cyclic;
 KW cell adhesion recognition sequence.
 XX Synthetic.
 XX US2002168761-A1.
 XX 14-NOV-2002.
 XX 24-JAN-2001; 2001US-00769145.
 XX 24-JAN-2000; 2000US-00491078.
 XX (GOUR/) GOUR B J.
 XX (BLAS/) BLASCHUK O W.
 XX (ALIA/) ALI A.
 XX (NIFF/) NI F.
 XX (CHEN/) CHEN Z.
 XX (MICH/) MICHAUD S D.
 XX (WANG/) WANG S.
 XX (HUZZ/) HU Z.
 XX GOUR BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;
 XX WPI; 2003-521524/49.
 XX Novel cell adhesion modulating agent for modulating cadherin-mediated
 PT intercellular adhesion, for enhancing wound healing, has three-
 PT dimensional structure similar to three-dimensional structure of cyclic
 PT peptide.
 XX Disclosure; Page 8; 309pp; English.
 XX The invention relates to a cell adhesion modulating agent which is a
 CC peptidomimetic having a three-dimensional structure of a cyclic peptide
 CC that comprises the sequence HAV within a cyclic peptide ring. The agent
 CC is useful for modulating classical cadherin-mediated intercellular
 CC adhesion, for reducing unwanted cellular adhesion in a mammal, for
 CC enhancing the delivery of a drug to a tumour, for inhibiting the
 CC development of cancer, for inhibiting angiogenesis, for enhancing drug
 CC delivery to the central nervous system, for enhancing wound healing, for
 CC enhancing the adhesion of foreign tissue implanted within a mammal, for
 CC modulating the immune system of a mammal, for increasing
 CC vasopermeability, for treating a demyelinating neurological disease, for
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC for inhibiting synaptic stability, for modulating neurite outgrowth, for
 CC treating spinal cord injuries and for treating macular degeneration. The
 CC cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or
 CC leukaemia. The agent is useful for treating skin disorders, acute B cell
 CC leukaemia, excessive immune reactions involving the humoral immune system
 CC and generation of immunoglobulins and diseases associated with excessive
 CC generation of T cells. This sequence represents a cadherin (CAD) cell
 CC adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the
 XX invention
 XX Sequence 6 AA;
 Query Match 100.0%; Score 34; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 1 CHAVC 5
 RESULT 32
 ADK13619
 ID ADK13619 standard; peptide; 6 AA.
 XX
 AC ADK13619;

XX 17-JUN-2004 (first entry)
 XX Cadherin-mediated cell adhesion-modulating peptidomimetic #78.
 DE XX
 XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
 KW angiogenesis; central nervous system; wound healing;
 KW foreign tissue adhesion; vasopermeability;
 KW demyelinating neurological disease; astrocyte; synaptic stability;
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.
 XX Synthetic.
 XX US2004058864-A1.
 XX 25-MAR-2004.
 XX 10-APR-2003; 2003US-00412701.
 XX 24-JAN-2000; 2000US-00491078.
 XX 24-JAN-2001; 2001US-00769145.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX GOUR BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;
 XX WPI; 2004-269836/25.
 XX New cell adhesion modulating agent, useful for treating or preventing
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing
 PT wound healing, treating a demyelinating neurological disease or treating
 PT spinal cord injuries.
 XX Disclosure; SEQ ID NO 85; 281pp; English.
 XX The invention relates to a cell adhesion-modulating agent. The invention
 CC also relates to methods for screening a candidate compound for the
 CC ability to modulate classical cadherin-mediated cell adhesion,
 CC identifying a compound that modulates classical cadherin-mediated cell
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
 CC to the central nervous system of a mammal, enhancing wound healing in a
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,
 CC modulating the immune system of a mammal, increasing vasopermeability in
 CC a mammal, treating a demyelinating neurological disease in a mammal,
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,
 CC treating spinal cord injuries in a mammal and treating macular
 CC degeneration in a mammal. The compounds are useful for inhibiting or
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating
 CC agents are useful for inhibiting the development of cancer, e.g. treating
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The
 CC agents are also useful in inhibiting angiogenesis, for enhancing the
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing
 CC to the central nervous system of a mammal, for enhancing wound healing in
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a
 CC mammal, for modulating the immune system of a mammal, for treating a
 CC demyelinating neurological disease (such as multiple sclerosis) in a
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for
 CC treating macular degeneration in a mammal. This sequence represents a
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a
 CC classical cadherin cell adhesion recognition (CAR) sequence.
 XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 34; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 2 CHAVC 6
|||||

RESULT 33
ADK13622
ID ADK13622 standard; peptide; 6 AA.

XX
AC ADK13622;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cadherin-mediated cell adhesion-modulating peptidomimetic #81.

XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
KW angiogenesis; central nervous system; wound healing;
KW foreign tissue adhesion; vasopermeability;
KW demyelinating neurological disease; astrocyte; synaptic stability;
KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;
KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;
KW multiple sclerosis; cystostatic; antiangiogenic; neuroprotective;
KW ophthalmological; Cell adhesion-modulating peptidomimetic;
KW cadherin cell adhesion recognition sequence; CAR; cyclic.

XX
OS Synthetic.
XX
PN US2004058864-A1.
XX
PD 25-MAR-2004.
XX
PF 10-APR-2003; 2003US-00412701.
XX
PS Disclosure; SEQ ID NO 88; 281pp; English.

XX The invention relates to a cell adhesion-modulating agent. The invention
CC also relates to methods for screening a candidate compound for the
CC ability to modulate classical cadherin-mediated cell adhesion,
CC identifying a compound that modulates classical cadherin-mediated cell
CC adhesion, modulating classical cadherin-mediated intercellular adhesion,
CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery
CC of a drug to a tumour in a mammal, inhibiting the development of a cancer
CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
CC to the central nervous system of a mammal, enhancing wound healing in a
CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,
CC modulating the immune system of a mammal, increasing vasopermeability in
CC a mammal, treating a demyelinating neurological disease in a mammal,
CC facilitating migration of an N-cadherin expressing cell on astrocytes,
CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,
CC treating spinal cord injuries in a mammal and treating macular
CC degeneration in a mammal. The compounds are useful for inhibiting or
CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating
CC agents are useful for inhibiting the development of cancer, e.g. treating

CC or preventing cancer and/or inhibiting metastasis. The cancer is a
CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The
CC agents are also useful in inhibiting angiogenesis, for enhancing the
CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in
CC to the central nervous system of a mammal, for enhancing drug delivery
CC a mammal, for enhancing adhesion of foreign tissue implanted within a
CC mammal, for modulating the immune system of a mammal, for treating a
CC demyelinating neurological disease (such as multiple sclerosis) in a
CC mammal, for inhibiting synaptic stability in a mammal, for modulating
CC neurite outgrowth, for treating spinal cord injuries in a mammal and for
CC treating macular degeneration in a mammal. This sequence represents a
CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a
CC classical cadherin cell adhesion recognition (CAR) sequence.

XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 34; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5
|||||

RESULT 34
ADK13623
ID ADK13623 standard; peptide; 6 AA.

XX
AC ADK13623;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cadherin-mediated cell adhesion-modulating peptidomimetic #82.

XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
KW angiogenesis; central nervous system; wound healing;
KW foreign tissue adhesion; vasopermeability;
KW demyelinating neurological disease; astrocyte; synaptic stability;
KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;
KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;
KW multiple sclerosis; cystostatic; antiangiogenic; neuroprotective;
KW ophthalmological; Cell adhesion-modulating peptidomimetic;
KW cadherin cell adhesion recognition sequence; CAR; cyclic.

XX
OS Synthetic.
XX
PN US2004058864-A1.
XX
PD 25-MAR-2004.
XX
PF 10-APR-2003; 2003US-00412701.
XX
PS Disclosure; SEQ ID NO 89; 281pp; English.

XX The invention relates to a cell adhesion-modulating agent. The invention
CC also relates to methods for screening a candidate compound for the
CC ability to modulate classical cadherin-mediated cell adhesion,
CC identifying a compound that modulates classical cadherin-mediated cell
CC adhesion, modulating classical cadherin-mediated intercellular adhesion,
CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery
CC of a drug to a tumour in a mammal, inhibiting the development of a cancer
CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
CC to the central nervous system of a mammal, enhancing wound healing in a
CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,
CC modulating the immune system of a mammal, increasing vasopermeability in
CC a mammal, treating a demyelinating neurological disease in a mammal,
CC facilitating migration of an N-cadherin expressing cell on astrocytes,
CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,
CC treating spinal cord injuries in a mammal and treating macular
CC degeneration in a mammal. The compounds are useful for inhibiting or
CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating
CC agents are useful for inhibiting the development of cancer, e.g. treating

CC identifying a compound that modulates classical cadherin-mediated cell
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
 CC to the central nervous system of a mammal, enhancing wound healing in a
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,
 CC modulating the immune system of a mammal, increasing vasopermeability in
 CC a mammal, treating a demyelinating neurological disease in a mammal,
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,
 CC treating spinal cord injuries in a mammal, and treating macular
 CC degeneration in a mammal. The compounds are useful for inhibiting or
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating
 CC agents are useful for inhibiting the development of cancer, e.g. treating
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The
 CC agents are also useful in inhibiting angiogenesis, for enhancing the
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in
 CC to the central nervous system of a mammal, for enhancing wound healing in
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a
 CC mammal, for modulating the immune system of a mammal, for treating a
 CC demyelinating neurological disease (such as multiple sclerosis) in a
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for
 CC treating macular degeneration in a mammal. This sequence represents a
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a
 CC classical cadherin cell adhesion recognition (CAR) sequence.

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 35

ADK13615

ID ADK13615 standard; peptide; 6 AA.

XX AC ADK13615;

XX DT 17-JUN-2004 (first entry)

XX DE Cadherin-mediated cell adhesion-modulating peptidomimetic #74.

XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
 KW angiogenesis; central nervous system; wound healing;
 KW foreign tissue adhesion; vasopermeability;
 KW demyelinating neurological disease; astrocyte; synaptic stability;
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.

XX OS Synthetic.

XX PN US2004058864-A1.

XX PD 25-MAR-2004.

XX PF 10-APR-2003; 2003US-00412701.

XX PR 24-JAN-2000; 2000US-00491078.

XX PR 24-JAN-2001; 2001US-00769145.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX

PI Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 PI Hu Z;

XX WPI; 2004-268836/25.

DR New cell adhesion modulating agent, useful for treating or preventing
 PT cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing
 PT wound healing, treating a demyelinating neurological disease or treating
 PT spinal cord injuries.

XX Claim 15; SEQ ID NO 81; 281pp; English.

XX The invention relates to a cell adhesion-modulating agent. The invention
 CC also relates to methods for screening a candidate compound for the
 CC ability to modulate classical cadherin-mediated cell adhesion,
 CC identifying a compound that modulates classical cadherin-mediated cell
 CC adhesion, modulating classical cadherin-mediated intercellular adhesion,
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
 CC to the central nervous system of a mammal, enhancing wound healing in a
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,
 CC modulating the immune system of a mammal, increasing vasopermeability in
 CC a mammal, treating a demyelinating neurological disease in a mammal,
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,
 CC treating spinal cord injuries in a mammal, and treating macular
 CC degeneration in a mammal. The compounds are useful for inhibiting or
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating
 CC agents are useful for inhibiting the development of cancer, e.g. treating
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The
 CC agents are also useful in inhibiting angiogenesis, for enhancing the
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in
 CC to the central nervous system of a mammal, for enhancing wound healing in
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a
 CC mammal, for modulating the immune system of a mammal, for treating a
 CC demyelinating neurological disease (such as multiple sclerosis) in a
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for
 CC treating macular degeneration in a mammal. This sequence represents a
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a
 CC classical cadherin cell adhesion recognition (CAR) sequence.

XX Sequence 6 AA;

Query Match 100.0%; Score 34; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 36

ADK13624

ID ADK13624 standard; peptide; 6 AA.

XX AC ADK13624;

XX DT 17-JUN-2004 (first entry)

XX DE Cadherin-mediated cell adhesion-modulating peptidomimetic #83.

XX Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
 KW angiogenesis; central nervous system; wound healing;
 KW foreign tissue adhesion; vasopermeability;
 KW demyelinating neurological disease; astrocyte; synaptic stability;
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 34; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||||
Db 1 CHAVC 5

RESULT 38
AAG65447
ID AAG65447 standard; peptide; 7 AA.
XX AC AAG65447;
DT 30-NOV-2001 (first entry)
XX Cyclic peptide with classical cadherin CAR sequence.
DE Cell adhesion; imidazole; peptidomimetic; cadherin; angiogenesis; CAR;
KW cytostatic; vulnery; immunomodulator; vasotropic; neuroprotective;
KW cerebroprotective; muscular; cyclic.
XX Synthetic.
OS
XX
XX
KH Location/Qualifiers
FT Modified-site 1
FT /note= "putative N-terminal acetylation or
FT alkoxybenzylolation"
FT Modified-site 7
FT /note= "putative C-terminal amide or ester"
XX
XX WO200153331-A2.
XX
XX 26-JUL-2001.
XX
XX 24-JAN-2001; 2001WO-US002508.
XX
XX 24-JAN-2000; 2000US-00491078.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
PI Hu Z;
XX
XX WPI; 2001-549899/61.
XX
XX Cell adhesion modulating agent used for enhancing delivery of drug to
XX tumor comprises imidazole compounds.
XX
XX Example; Page 413; 436pp; English.
XX
XX The invention relates to cell adhesion modulating agents that comprise
XX imidazole compounds of specified formulae that are peptidomimetics of
XX cyclic peptides. The peptidomimetics have a structure similar to that of
XX a cyclic peptide that comprises a cadherin cell recognition sequence HAV.
XX The agents are used for modulating classical cadherin mediated
XX intercellular adhesion, reducing unwanted cellular adhesion, enhancing
XX delivery of a drug to a tumor, inhibiting development of cancer,
XX inhibiting angiogenesis, enhancing drug delivery to the CNS, enhancing
XX wound healing, modulating the immune system, increasing vasopermeability,
XX treating demyelinating disease, facilitating migration of an N-cadherin
XX expressing cell on astrocytes, inhibiting synaptic stability, modulating
XX neurite outgrowth, and treating spinal cord injuries and macular
XX degeneration. The present sequence represents a cyclic peptide with
XX classical cadherin cell adhesion recognition (CAR) sequence
XX SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 4; Length 7;

```

Db          |||||
            1 CHAVC 5

RESULT 40
AAM47556
ID AAM47556 standard; peptide; 7 AA.
XX
AC AAM47556;
XX
DT 12-FEB-2002 (first entry)
XX
DE Cyclic peptide endothelial cell adhesion modulator #17.
XX
KW Cadherin; cytostatic; gynecological; endometriosis;
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
KW cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Linked to residue 7 to form a cyclic peptide, N-
FT terminal acetyl or N-terminal CH3-SO2 group"
FT Modified-site 7
FT /note= "linked to residue 1 to form a cyclic peptide, C-
FT terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Claim 6; Page 64; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence is one such
XX modulating peptide
XX
XX Sequence 7 AA;
XX
Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy' 1 CHAVC 5
      |||||
      1 CHAVC 5

RESULT 41

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AAM47563
ID AAM47563 standard; peptide; 7 AA.
XX
XX AAM47563;
XX
DT 12-FEB-2002 (first entry)
XX
DE Cyclic peptide endothelial cell adhesion modulator #39.
XX
KW Cadherin; cytostatic; gynecological; endometriosis;
KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
KW cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Linked to residue 7 to form a cyclic peptide, N-
FT terminal CH3-SO2 group"
FT Modified-site 7
FT /note= "Linked to residue 1 to form a cyclic peptide, C-
FT terminal amide"
XX
XX WO200177146-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US011669.
XX
XX 07-APR-2000; 2000US-00544782.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ, Farookhi R, Ali A;
XX WPI; 2002-049129/06.
XX
XX Modulating endothelial cell adhesion for inhibiting development of
XX endometriosis, increasing blood flow to tumor in a mammal, by contacting
XX cell with a cyclic peptide having cadherin cell adhesion recognition
XX sequence.
XX
XX Disclosure; Page 5; 139pp; English.
XX
XX The present invention relates to a method for modulating endothelial cell
XX adhesion. The method comprises contacting an endothelial cell with a
XX modulating peptide comprising a cadherin cell adhesion recognition
XX sequence (His Ala Val) within a cyclic peptide ring. The method is useful
XX for inhibiting angiogenesis, increasing vasopermeability, increasing
XX blood flow to a tumour, disrupting neovasculture and inhibiting the
XX development of endometriosis in a mammal. The modulating peptide reduces
XX unwanted endothelial adhesion occurring between tumour cells, tumour
XX cells and normal cells, normal cells as a result of surgery, injury,
XX chemotherapy, disease and inflammation. The present sequence is one such
XX modulating peptide
XX
XX Sequence 7 AA;
XX
Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
     |||||
     3 CHAVC 7

RESULT 42
AAM47557
ID AAM47557 standard; peptide; 7 AA.
XX
XX AAM47557;
XX

```


ABO43615	Query Match	100.0%;	Score 34;	DB 7;	Length 7;
ID ABO43615 standard; peptide; 7 AA.	Best Local Similarity	100.0%;	Pred. No. 1.8e+06;		
XX	Matches 5;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
AC ABO43615;					
XX					
DT 25-SEP-2003 (first entry)	QY 1 CHAVC 5				
XX					
DE	Db 1 CHAVC 5				
XX					
DE					
XX					
KW	RESULT 45				
KN	ADK13620				
XX	ID ADK13620 standard; peptide; 7 AA.				
AC	XX				
XX	ADK13620;				
DT 17-JUN-2004 (first entry)	XX				
XX	XX				
DE	Cadherin-mediated cell adhesion-modulating peptidomimetic #79.				
XX					
KW	Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;				
KN	angiogenesis; central nervous system; wound healing;				
XX	foreign tissue adhesion; vasopermeability;				
KW	demyelinating neurological disease; astrocyte; synaptic stability;				
KN	neurite outgrowth; spinal cord injury; macular degeneration; metastasis;				
KW	bladder; tumour; ovary; melanoma; carcinoma; leukaemia;				
XX	multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;				
KW	ophthalmological; Cell adhesion-modulating peptidomimetic;				
XX	cadherin cell adhesion recognition sequence; CAR; cyclic.				
OS	Synthetic.				
XX					
PN	US2004058864-A1.				
XX					
PD	25-MAR-2004.				
XX					
PF	10-APR-2003; 2003US-00412701.				
XX					
PR	24-JAN-2000; 2000US-00491078.				
XX	24-JAN-2001; 2001US-00769145.				
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.				
XX					
PI	Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;				
XX	Hu Z;				
DR	WPI; 2004-269836/25.				
XX					
PT	New cell adhesion modulating agent, useful for treating or preventing				
XX	cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing				
PT	wound healing, treating a demyelinating neurological disease or treating				
XX	spinal cord injuries.				
PS	Disclosure; SEQ ID NO 86; 281pp; English.				
XX					
CC	The invention relates to a cell adhesion-modulating agent. The invention				
CC	also relates to methods for screening a candidate compound for the				
CC	ability to modulate classical cadherin-mediated cell adhesion,				
CC	identifying a compound that modulates classical cadherin-mediated cell				
CC	adhesion, modulating classical cadherin-mediated intercellular adhesion,				
CC	reducing unwanted cellular adhesion in a mammal, enhancing the delivery				
CC	of a drug to a tumour in a mammal, inhibiting the development of a cancer				
CC	in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery				
CC	to the central nervous system of a mammal, enhancing wound healing in a				
CC	mammal, enhancing adhesion of foreign tissue implanted within a mammal,				
CC	modulating the immune system of a mammal, increasing vasopermeability in				
CC	a mammal, treating a demyelinating neurological disease in a mammal,				
CC	facilitating migration of an N-cadherin expressing cell on astrocytes,				
CC	inhibiting synaptic stability in a mammal, modulating neurite outgrowth,				
CC	treating spinal cord injuries in a mammal and treating macular				
CC	degeneration in a mammal. The compounds are useful for inhibiting or				
CC	enhancing cadherin-mediated cell adhesion. The cell adhesion modulating				
CC	agents are useful for inhibiting the development of cancer, e.g. treating				
CC	or preventing cancer and/or inhibiting metastasis. The cancer is a				
ABO43615	Cadherin; CAD; extracellular domain; cell adhesion; peptidomimetic;				
XX	cadherin-mediated intercellular adhesion; tumour; cancer; angiogenesis;				
XX	central nervous system; wound healing; vasopermeability; N-cadherin;				
AC ABO43615;	demyelinating neurological disease; astrocyte; synaptic stability; ovary;				
XX	neurite outgrowth; spinal cord injury; macular degeneration; bladder;				
DT 25-SEP-2003 (first entry)	XX				
XX	melanoma; carcinoma; leukaemia; skin disorder; acute B cell leukaemia;				
DE	immune reaction; immunoglobulin; T cell generation; CAR; cyclic;				
XX	cell adhesion recognition sequence.				
OS	Synthetic.				
XX					
PN	US2002168761-A1.				
XX					
PD	14-NOV-2002.				
XX					
PF	24-JAN-2001; 2001US-00769145.				
XX					
PR	24-JAN-2000; 2000US-00491078.				
XX					
PA	(GOUR/) GOUR B J.				
XX	(BLAS/) BLASCHUK O W.				
PI	(ALIA/) ALI A.				
XX	(NIFE/) NI F.				
PA	(CHEN/) CHEN Z.				
XX	(MICH/) MICHAUD S D.				
PA	(WANG/) WANG S.				
XX	(HUZZ/) HU Z.				
PI	Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;				
XX	Hu Z;				
DR	WPI; 2003-521524/49.				
XX					
PT	Novel cell adhesion modulating agent for modulating cadherin-mediated				
XX	intercellular adhesion, for enhancing wound healing, has three-				
PT	dimensional structure similar to three-dimensional structure of cyclic				
XX	peptide.				
PS	Disclosure; Page 7; 309pp; English.				
XX					
CC	The invention relates to a cell adhesion modulating agent which is a				
CC	peptidomimetic having a three-dimensional structure of a cyclic peptide				
CC	that comprises the sequence HAV within a cyclic peptide ring. The agent				
CC	is useful for modulating classical cadherin-mediated intercellular				
CC	adhesion, for reducing unwanted cellular adhesion in a mammal, for				
CC	enhancing the delivery of a drug to a tumour, for inhibiting the				
CC	development of cancer, for inhibiting angiogenesis, for enhancing drug				
CC	delivery to the central nervous system, for enhancing wound healing, for				
CC	enhancing the adhesion of foreign tissue implanted within a mammal, for				
CC	modulating the immune system of a mammal, for increasing				
CC	vasopermeability, for treating a demyelinating neurological disease, for				
CC	facilitating migration of an N-cadherin expressing cell on astrocytes,				
CC	for inhibiting synaptic stability, for modulating neurite outgrowth, for				
CC	treating spinal cord injuries and for treating macular degeneration. The				
CC	cancer is a bladder tumour, ovarian tumour, melanoma, carcinoma or				
CC	leukaemia. The agent is useful for treating skin disorders, acute B cell				
CC	leukaemia, excessive immune reactions involving the humoral immune system				
CC	and generation of immunoglobulins and diseases associated with excessive				
CC	generation of T cells. This sequence represents a cadherin (CAD) cell				
CC	adhesion recognition (CAR) sequence cyclic peptide peptidomimetic of the				
XX	invention				
SQ	Sequence 7 AA;				

CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The
 CC agents are also useful in inhibiting angiogenesis, for enhancing the
 CC delivery of a drug to a tumour in a mammal, for enhancing drug delivery
 CC to the central nervous system of a mammal, for enhancing wound healing in
 CC a mammal, for enhancing adhesion of foreign tissue implanted within a
 CC mammal, for modulating the immune system of a mammal, for treating a
 CC demyelinating neurological disease (such as multiple sclerosis) in a
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for
 CC treating macular degeneration in a mammal. This sequence represents a
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a
 CC classical cadherin cell adhesion recognition (CAR) sequence.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 1 CHAVC 5
 |||||
 |||||
 RESULT 46
 ADK13621
 ID ADK13621 standard; peptide; 7 AA.
 XX
 AC ADK13621;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Cadherin-mediated cell adhesion-modulating peptidomimetic #80.
 XX
 KW Cell adhesion-modulating agent; cadherin-mediated cell adhesion; cancer;
 KW angiogenesis; central nervous system; wound healing;
 KW foreign tissue adhesion; vasopermeability;
 KW demyelinating neurological disease; astrocyte; synaptic stability;
 KW neurite outgrowth; spinal cord injury; macular degeneration; metastasis;
 KW bladder; tumour; ovary; melanoma; carcinoma; leukaemia;
 KW multiple sclerosis; cytostatic; antiangiogenic; neuroprotective;
 KW ophthalmological; Cell adhesion-modulating peptidomimetic;
 KW cadherin cell adhesion recognition sequence; CAR; cyclic.
 XX
 OS Synthetic.
 XX
 XX US2004058864-A1.
 XX
 XX 25-MAR-2004.
 XX
 XX 10-APR-2003; 2003US-00412701.
 XX
 XX 24-JAN-2000; 2000US-00491078.
 XX
 XX 24-JAN-2001; 2001US-00769145.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Gour BJ, Blaschuk OW, Ali A, Ni F, Chen Z, Michaud SD, Wang S;
 XX Hu Z;
 XX
 XX WPI; 2004-268836/25.
 XX
 XX New cell adhesion modulating agent, useful for treating or preventing
 XX cancer and/or inhibiting metastasis, inhibiting angiogenesis, enhancing
 XX wound healing, treating a demyelinating neurological disease or treating
 XX spinal cord injuries.
 XX
 XX Disclosure; SEQ ID NO 87; 281pp; English.
 XX
 XX The invention relates to a cell adhesion-modulating agent. The invention
 XX also relates to methods for screening a candidate compound for the
 XX ability to modulate classical cadherin-mediated cell adhesion,
 XX identifying a compound that modulates classical cadherin-mediated cell

CC adhesion, modulating classical cadherin-mediated intercellular adhesion,
 CC reducing unwanted cellular adhesion in a mammal, enhancing the delivery
 CC of a drug to a tumour in a mammal, inhibiting the development of a cancer
 CC in a mammal, inhibiting angiogenesis in a mammal, enhancing drug delivery
 CC to the central nervous system of a mammal, enhancing wound healing in a
 CC mammal, enhancing adhesion of foreign tissue implanted within a mammal,
 CC modulating the immune system of a mammal, increasing vasopermeability in
 CC a mammal, treating a demyelinating neurological disease in a mammal,
 CC facilitating migration of an N-cadherin expressing cell on astrocytes,
 CC inhibiting synaptic stability in a mammal, modulating neurite outgrowth,
 CC treating spinal cord injuries in a mammal and treating macular
 CC degeneration in a mammal. The compounds are useful for inhibiting or
 CC enhancing cadherin-mediated cell adhesion. The cell adhesion modulating
 CC agents are useful for inhibiting the development of cancer, e.g. treating
 CC or preventing cancer and/or inhibiting metastasis. The cancer is a
 CC bladder tumour, ovarian tumour, melanoma, carcinoma or leukaemia. The
 CC agents are also useful in inhibiting angiogenesis, for enhancing the
 CC delivery of a drug to a tumour in a mammal, for enhancing wound healing in
 CC to the central nervous system of a mammal, for enhancing drug delivery
 CC in a mammal, for enhancing adhesion of foreign tissue implanted within a
 CC mammal, for modulating the immune system of a mammal, for treating a
 CC demyelinating neurological disease (such as multiple sclerosis) in a
 CC mammal, for inhibiting synaptic stability in a mammal, for modulating
 CC neurite outgrowth, for treating spinal cord injuries in a mammal and for
 CC treating macular degeneration in a mammal. This sequence represents a
 CC cadherin-mediated cell adhesion-modulating peptidomimetic, comprising a
 CC classical cadherin cell adhesion recognition (CAR) sequence.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 2 CHAVC 6
 |||||
 |||||
 RESULT 47
 AAM47562
 ID AAM47562 standard; peptide; 8 AA.
 XX
 AC AAM47562;
 XX
 XX 12-FEB-2002 (first entry)
 XX
 DE Cyclic peptide endothelial cell adhesion modulator #22.
 XX
 KW Cadherin; cytostatic; gynecological; endometriosis;
 KW endothelial cell adhesion; angiogenesis; vasopermeability; tumour;
 KW cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 1
 XX /note= "Linked to residue 8 to form a cyclic peptide, N-
 XX terminal acetyl or N-terminal CH3-SO2 group"
 XX Modified-site 8
 XX /note= "Linked to residue 1 to form a cyclic peptide, C-
 XX terminal amide"
 XX
 XX WO200177146-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 09-APR-2001; 2001WO-US011669.
 XX
 XX 07-APR-2000; 2000US-00544782.
 XX
 XX (UYMC-) UNIV MCGILL.

PI Blaschuk OW, Gour BJ, Farookhi R, Ali A;
 DR WPI; 2002-049129/06.
 XX
 XX Modulating endothelial cell adhesion for inhibiting development of
 PT endometriosis, increasing blood flow to tumor in a mammal, by contacting
 PT cell with a cyclic peptide having cadherin cell adhesion recognition
 PT sequence.
 XX
 XX Claim 6; Page 64; 139pp; English.
 PS
 PS The present invention relates to a method for modulating endothelial cell
 CC adhesion. The method comprises contacting an endothelial cell with a
 CC modulating peptide comprising a cadherin cell adhesion recognition
 CC sequence (His Ala Val) within a cyclic peptide ring. The method is useful
 CC for inhibiting angiogenesis, increasing vasopermeability, increasing
 CC blood flow to a tumour, disrupting neovasculature and inhibiting the
 CC development of endometriosis in a mammal. The modulating peptide reduces
 CC unwanted endothelial adhesion occurring between tumour cells, tumour
 CC cells and normal cells, normal cells as a result of surgery, injury,
 CC chemotherapy, disease and inflammation. The present sequence is one such
 CC modulating peptide
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 34; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 3 CHAVC 7
 RESULT 48
 AAY68110
 ID AAY68110 standard; protein; 61 AA.
 XX
 AC AAY68110;
 XX
 DT 13-APR-2000 (first entry)
 XX
 DE Kunitz protease inhibitor variant TW6151.
 XX
 KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
 KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
 KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
 KW anti-arthritis; thrombolytic; antirheumatic; antipsoriatic;
 KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
 KW rheumatoid arthritis; myocardial infarction; transplant rejection.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9963090-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 03-JUN-1999; 99WO-US012276.
 XX
 PR 03-JUN-1998; 98US-0087885P.
 XX
 PA (SCIO-) SCIOS INC.
 XX
 PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
 PI Pollitt NS, Lam AO;
 XX
 DR WPI; 2000-105699/09.
 XX
 XX Novel enzyme inhibitors especially used to reduce postoperative bleeding.
 PT
 PS Example 4; Fig 64; 151pp; English.
 XX

CC The present invention describes protease inhibitors that are analogues of
 CC the Kunitz protease inhibitor (KPI) domain of the amyloid precursor
 CC protein. The protease inhibitors can be used to treat or prevent
 CC disorders associated with increased activity of serine proteases,
 CC specifically blood loss during surgery (particularly cardiopulmonary
 CC bypass surgery where plasma proteases are activated by contact with
 CC surfaces in the heart-lung machine), but also other conditions such as
 CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; psoriasis;
 CC myocardial infarction; and transplant rejection. They are also for organ
 CC preservation and to promote wound healing. In vitro the protease
 CC inhibitors may be used to inhibit serine proteases during preparation of
 CC cell extracts. The protease inhibitors are based on a human peptide
 CC sequence so are unlikely to be immunogenic, can be produced at high
 CC levels in recombinant expression systems, and can inhibit a wide range of
 CC serine proteases. They are more potent or specific than known inhibitors.
 CC The present sequence represents a KPI variant which is given in an
 XX example from the present invention
 SQ Sequence 61 AA;
 Query Match 100.0%; Score 34; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 53 CHAVC 57
 RESULT 49
 AAY68085
 ID AAY68085 standard; protein; 61 AA.
 XX
 AC AAY68085;
 XX
 DT 13-APR-2000 (first entry)
 XX
 DE Kunitz protease inhibitor variant TW6182.
 XX
 KW Kunitz protease inhibitor; KPI; serine protease; kallikrein; plasmin;
 KW amyloid precursor protein; coagulation factor; blood loss; cardiant;
 KW cardiopulmonary bypass surgery; anticoagulant; anti-inflammatory;
 KW anti-arthritis; thrombolytic; antirheumatic; antipsoriatic;
 KW immunosuppressant; pancreatitis; deep vein thrombosis; psoriasis;
 KW rheumatoid arthritis; myocardial infarction; transplant rejection.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9963090-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 03-JUN-1999; 99WO-US012276.
 XX
 PR 03-JUN-1998; 98US-0087885P.
 XX
 PA (SCIO-) SCIOS INC.
 XX
 PI White RT, Damm D, Lesikar DD, Mcfadden K, Garrick BL, Lucas AB;
 PI Pollitt NS, Lam AO;
 XX
 DR WPI; 2000-105699/09.
 XX
 XX Novel enzyme inhibitors especially used to reduce postoperative bleeding.
 PT
 PS Example 4; Fig 64; 151pp; English.
 XX

CC bypass surgery where plasma proteases are activated by contact with
 CC surfaces in the heart-lung machine), but also other conditions such as
 CC pancreatitis; deep vein thrombosis; rheumatoid arthritis; peoriasis;
 CC myocardial infarction; and transplant rejection. They are also for organ
 CC preservation and to promote wound healing. In vitro the protease
 CC inhibitors may be used to inhibit serine proteases during preparation of
 CC cell extracts. The protease inhibitors are based on a human peptide
 CC sequence so are unlikely to be immunogenic, can be produced at high
 CC levels in recombinant expression systems, and can inhibit a wide range of
 CC serine proteases. They are more potent or specific than known inhibitors.
 CC The present sequence represents a KPI variant which is given in an
 CC example from the present invention
 XX

SQ Sequence 61 AA;

Query Match 100.0%; Score 34; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 53 CHAVC 57

RESULT 50

ID AAU28273 standard; protein; 121 AA.

AC AAU28273;

DT 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 630.

KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.

OS Homo sapiens.

PN WO200166689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US004942.

PR 07-MAR-2000; 2000US-00519705.

PR 19-MAY-2000; 2000US-00574454.

PR 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00616847.

PR 19-SEP-2000; 2000US-00655363.

PR 20-OCT-2000; 2000US-00693267.

XX (HYSE-) HYSEQ INC.

FA Tang YT, Liu C, Arundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanan RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.

DR N-PSDB; AAS45173.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders.
 XX
 PS Example 2; SEQ ID NO 630; 107pp; English.
 XX

CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,
 CC or periodontal disease. Furthermore, (I) is also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biohythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention
 XX

SQ Sequence 121 AA;

Query Match 100.0%; Score 34; DB 4; Length 121;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 61 CHAVC 65

RESULT 51

AAG38298

ID AAG38298 standard; protein; 198 AA.

AC AAG38298;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 47228.

XX Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135829P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
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PR	01-JUL-1999;	99US-0141842P.	PR	20-SEP-1999;	99US-0154779P.
PR	01-JUL-1999;	99US-0142154P.	PR	22-SEP-1999;	99US-0155139P.
PR	02-JUL-1999;	99US-0142055P.	PR	23-SEP-1999;	99US-0155486P.
PR	06-JUL-1999;	99US-0142390P.	PR	24-SEP-1999;	99US-0155659P.
PR	08-JUL-1999;	99US-0142803P.	PR	28-SEP-1999;	99US-0156458P.
PR	09-JUL-1999;	99US-0142920P.	PR	29-SEP-1999;	99US-0156596P.
PR	12-JUL-1999;	99US-0142977P.	PR	04-OCT-1999;	99US-0157117P.
PR	13-JUL-1999;	99US-0143542P.	PR	05-OCT-1999;	99US-0157753P.
PR	14-JUL-1999;	99US-0143624P.	PR	06-OCT-1999;	99US-0157865P.
PR	15-JUL-1999;	99US-0144005P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144085P.	PR	08-OCT-1999;	99US-0158232P.
PR	16-JUL-1999;	99US-0144086P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144325P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144333P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159330P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144632P.	PR	18-OCT-1999;	99US-0159584P.
PR	20-JUL-1999;	99US-0144884P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-0160767P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160768P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145089P.			

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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 25-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161362P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 34; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 106 CHAVC 110

RESULT 54
AAG07318
ID AAG07318 standard; protein; 244 AA.
XX AC AAG07318;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 4427.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126264P.
PR 23-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
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PR 18-JUN-1999; 99US-0139458P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
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PR 27-JUL-1999; 99US-0145913P.
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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146336P.
PR 02-AUG-1999; 99US-0146338P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
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PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 21-OCT-1999; 99US-0160741P.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.

PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 34; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 106 CHAVC 110

RESULT 55
ABB67444
ID ABB67444 standard; protein; 380 AA.
XX AC ABB67444;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 29124.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX FA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL11547.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions.
XX PS Disclosure; SEQ ID NO 29124; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (AB16176-AB160511), expressed DNA
sequences (AB161840-AB16175) and the encoded proteins (ABBS7737-
ABBS72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 380 AA;

Query Match 100.0%; Score 34; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||||
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Db          318 CHAVC 322

RESULT 56
ABB83912
ID ABB83912 standard; protein; 381 AA.
XX
XX ABB83912;
AC
XX
XX 14-OCT-2002 (first entry)
XX
XX Drosophila melanogaster Can 1 SEQ ID NO 8.
XX
XX Human; Can 1; antiinfertility; gynaecological; infertility;
XX prematute ovarian failure; menopause; Sertoli Cell only syndrome;
XX GenBank reference AAF54486.
XX
XX Drosophila melanogaster.
OS
XX
XX US2002119929-A1.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 02-NOV-2001; 2001US-00003806.
PF
XX
XX 03-NOV-2000; 2000US-0245872P.
PR
XX
XX (BISH/) BISHOP C E.
PA
XX (AGOU/) AGOULNIK A I.
PA
XX (ZHUQ/) ZHU Q.
XX
XX Bishop CE, AgoulNIK AI, Zhu Q;
PI
XX
XX WPI; 2002-618953/66.
DR
XX
XX A nucleic acid molecule (I) encoding a Can 1 polypeptide used in treating
XX infertility.
PT
XX
XX Disclosure; Page; 45pp; English.
PS
XX
XX The invention relates to a nucleic acid molecule (I) encoding a Can 1
XX polypeptide. The Can 1 nucleic acid molecule is used to diagnose or treat
XX infertility or premature ovarian failure or Sertoli Cell only syndrome in
XX a mammal. The present sequence is that of the Drosophila melanogaster Can
XX 1 protein of the invention. Note: The present sequence is not given in
XX the printed specification but was obtained through the GenBank reference
XX AAF54486
CC
XX
XX Sequence 381 AA;
SQ
Query Match          100.0%; Score 34; DB 5; Length 381;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
        |||||
Db      338 CHAVC 342

RESULT 57
ADE97396
ID ADE97396 standard; protein; 537 AA.
XX
XX ADE97396;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Porcine intercellular adhesion molecule-1 precursor protein.
DE
XX
XX immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;
XX virucide; antibacterial; anthrax; rhinovirus infection; common cold;
XX intercellular adhesion molecule; ICAM-1; human; pig; porcine.
XX

Sus scrofa.
OS
XX
XX WO2003064992-A2.
PN
XX
XX 07-AUG-2003.
PD
XX
XX 25-OCT-2002; 2002WO-US034197.
PF
XX
XX 26-OCT-2001; 2001US-00047542.
PR
XX
XX (PLAN-) PLANET BIOTECHNOLOGY INC.
XX (LARR/) LARRICK J W.
XX (WYCO/) WYCOFF K L.
PA
XX
XX Larrick JW, Wycoff KL;
PI
XX
XX WPI; 2003-636816/60.
DR
XX
XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises
XX chimeric toxin receptor protein linked to immunoglobulin heavy chain, and
XX J chain and secretory component associated with the chimeric toxin
XX receptor protein.
PT
XX
XX Disclosure; SEQ ID NO 74; 288pp; English.
PS
XX
XX The invention relates to a novel immunoadhesin comprising a chimeric
XX toxin receptor protein consisting of a toxin receptor protein linked to
XX at least a portion of an immunoglobulin heavy chain with a J (joining)
XX chain and secretory component (SC) associated with the chimeric toxin
XX receptor protein. The immunoadhesin comprises a chimeric bacterial or
XX viral toxin receptor protein and the immunoadhesin has plant-specific
XX glycosylation. The immunoadhesin of the invention demonstrates virucide
XX and antibacterial activities and may be useful for reducing the binding
XX of a viral or bacterial antigen to a host cell and thus for treating or
XX preventing anthrax, as well as human rhinovirus infection which results
XX in the common cold. The current sequence is that of the porcine
XX immunoadhesin-related protein of the invention.
CC
XX
XX Sequence 537 AA;
SQ
Query Match          100.0%; Score 34; DB 7; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
        |||||
Db      96 CHAVC 100

RESULT 58
ADB74464
ID ADB74464 standard; protein; 542 AA.
XX
XX ADB74464;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Mycobacterium leprae non-naturally occurring peptide #164.
DE
XX
XX Non-naturally occurring peptide; anion pump protein; tuberculosis;
XX hypersensitivity reaction; tuberculostatic.
XX
XX Mycobacterium leprae.
OS
XX
XX US6583266-B1.
PN
XX
XX 24-JUN-2003.
PD
XX
XX 16-SEP-1994; 94US-00311731.
PF
XX
XX 19-AUG-1993; 93US-00109181.
PR
XX
XX 22-OCT-1993; 93US-00142558.
XX

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PA (GENO-) GENOME THERAPEUTICS CORP.
XX Smith DR, Mao J;
PI WPI; 2003-656441/62.
XX New Mycobacterium tuberculosis anion pump peptide useful for as
PT tuberculosis vaccine and diagnosis of tuberculosis infection.
XX Disclosure; SEQ ID NO 213; 26pp; English.
XX
CC The invention relates to a non-naturally occurring peptide of
CC Mycobacterium tuberculosis comprising an amino acid sequence
CC corresponding to an anion pump protein. The invention also relates to a
CC non-naturally occurring nucleic acid corresponding to a DNA sequence of
CC Mycobacterium tuberculosis or Mycobacterium leprae. The new peptide is
CC useful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
CC leprae or for screening for new tuberculosis drugs. Purified proteins
CC derived from the sequences of the invention may elicit a specific immune
CC response. The peptide may also be used to detect hypersensitivity
CC reactions of individuals exposed to Mycobacterium tuberculosis or
CC Mycobacterium leprae. The proteins and peptides may be affixed to solid
CC supports to detect antibodies typical of hypersensitivity reactions, from
CC a patient's sera. This sequence represents Mycobacterium leprae non-
CC naturally occurring peptide of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 542 AA;
SQ
Query Match 100.0%; Score 34; DB 7; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT 59
ADK16783
ID ADK16783 standard; protein; 75 AA.
AC ADK16783;
XX 06-MAY-2004 (first entry)
XX
XX Nanoarchaeum equitans cancer-associated (CA) protein #367.
XX cancer-associated gene; CA gene; cancer; carcinoma; lymphoma; leukaemia.
XX Nanoarchaeum equitans.
XX WO2003093434-A2.
XX 13-NOV-2003.
XX 01-MAY-2003; 2003WO-US013699.
XX 01-MAY-2002; 2002US-0377447P.
XX (DIVE-) DIVERSA CORP.
XX Stetter KO, Waters E, Kretz K, Podar M, Richardson T,
PI Noordewier M;
XX WPI; 2004-053041/05.
DR N-PSDB; ADK16782.
XX
XX New recombinant cancer-associated genes, such as KCMJ9, useful for
PT diagnosing or treating carcinoma, e.g. breast, colon, rectal, pancreatic,
PT cervical, or skin cancers, lymphomas, or leukemia.
XX
XX Claim 64; SEQ ID NO 735; 251pp; English.
XX
XX The invention comprises then amino acid and coding sequences of cancer-
CC associated (CA) genes isolated from Nanoarchaeum equitans. The invention
CC also comprises the Nanoarchaeum equitans genome. The DNA and protein
CC sequences of the invention are useful for diagnosing and treating cancer
CC (e.g. carcinoma, lymphoma, or leukaemia). The present amino acid sequence
CC represents a Nanoarchaeum equitans CA protein of the invention.
XX
XX Sequence 75 AA;
SQ
Query Match 97.1%; Score 33; DB 8; Length 75;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 17 CHAIC 21
RESULT 60
AAU50581
ID AAU50581 standard; protein; 176 AA.
XX AAU50581;
XX 13-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein #11477.
DE
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
OS
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59549.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 11776; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 176 AA;
 SQ

Query Match 97.1%; Score 33; DB 4; Length 176;
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 Db 53 CHAIC 57
 |||:|

RESULT 61
 ABM47100
 ID ABM47100 standard; protein; 176 AA.
 XX
 AC ABM47100;
 XX
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #11776.
 XX
 XX
 KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 XX 11-OCT-2002; 2002WO-US032727.
 XX
 XX 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglass J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64478.
 XX

CC New Propionibacterium acnes polypeptides and polynucleotides encoding the
 CC polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 CC or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 11776; 1481pp; English.
 XX

CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC polynucleotide; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a

CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 176 AA;
 SQ

Query Match 97.1%; Score 33; DB 6; Length 176;
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 Db 53 CHAIC 57
 |||:|

RESULT 62
 ABB92762
 ID ABB92762 standard; protein; 428 AA.
 XX
 AC ABB92762;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Herbicidally active polypeptide SEQ ID NO 1973.
 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200210210-A2.
 XX
 PD 07-FEB-2002.
 XX
 XX 28-AUG-2001; 2001WO-EP009892.
 XX
 XX 28-AUG-2001; 2001WO-EP009892.
 PR (FARB) BAYER AG.
 XX
 PI Tietjen K, Weidler M;
 XX
 DR WPI; 2002-269010/31.
 XX

CC Identifying plant target proteins for herbicidally active compounds,
 CC comprising aligning and comparing nucleic acid or amino acid sequences
 CC from plant with nucleic acid or amino acid sequences from non-plant
 CC organisms.
 XX
 PS Claim 5; SEQ ID NO 1973; 261pp + Sequence Listing; English.
 XX

CC The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 XX
 SQ Sequence 428 AA;
 XX

Query Match 97.1%; Score 33; DB 5; Length 428;

Best Local Similarity 80.0%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 1 CHAVC 5
Db 153 CHAIC 157

RESULT 63
AAY72708
ID AAY72708 standard; protein; 672 AA.
XX AC AAY72708;
XX AC
XX AC
DT 06-AUG-2003 (revised)
DT 31-MAY-2001 (first entry)
XX Parvovirus non-structure protein 1 (NS1) variant (T394A).
XX NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
XX tumoural disease; gene therapy; mutant; mutein; variant.
XX Parvovirus.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 394 /note= "Wild type Thr substituted with Ala"
FT
XX EPI077260-A1.
XX 21-FEB-2001.
XX 13-AUG-1999; 99EP-00115161.
XX 13-AUG-1999; 99EP-00115161.
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Nueesch J, Rommelaere J;
XX WPI; 2001-212717/22.
XX N-PSDB; AAD02803.
XX Novel parvovirus non-structure protein variant, useful for treating
XX tumoral diseases, has a shifted equilibrium between DNA replication and
XX transcription activities, and cytotoxic activity.
XX Claim 6; Page 25-27; 41pp; English.
XX The present sequence is parvovirus non-structure protein 1 (NS1) variant
XX (T394A). The invention relates to the variants of the parvovirus non-
XX structure protein (NS1) having a shifted equilibrium between the DNA
XX replication and transcription activities, and the cytotoxicity activity.
XX These variants are useful as toxins for treating tumoural diseases. The
XX variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
XX 2003 to correct OS field.)
XX SQ Sequence 672 AA;

Query Match 97.1%; Score 33; DB 4; Length 672;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 378 CHAIC 382

RESULT 64
AAY72710
ID AAY72710 standard; protein; 672 AA.
XX AC AAY72710;
XX AC
XX AC
DT 06-AUG-2003 (revised)
DT 31-MAY-2001 (first entry)
XX Parvovirus non-structure protein 1 (NS1) variant (T463A).
XX NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
XX tumoural disease; gene therapy; mutant; mutein; variant.
XX Parvovirus.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 463 /note= "Wild type Thr substituted with Ala"
FT
XX EPI077260-A1.
XX 21-FEB-2001.
XX 13-AUG-1999; 99EP-00115161.
XX 13-AUG-1999; 99EP-00115161.
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Nueesch J, Rommelaere J;
XX WPI; 2001-212717/22.
XX N-PSDB; AAD02805.
XX Novel parvovirus non-structure protein variant, useful for treating
XX tumoral diseases, has a shifted equilibrium between DNA replication and
XX transcription activities, and cytotoxic activity.
XX Claim 6; Page 30-32; 41pp; English.
XX The present sequence is parvovirus non-structure protein 1 (NS1) variant
XX (T463A). The invention relates to the variants of the parvovirus non-
XX structure protein (NS1) having a shifted equilibrium between the DNA
XX replication and transcription activities, and the cytotoxicity activity.
XX These variants are useful as toxins for treating tumoural diseases. The
XX variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
XX 2003 to correct OS field.)
XX SQ Sequence 672 AA;

Query Match 97.1%; Score 33; DB 4; Length 672;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 378 CHAIC 382

RESULT 65
AAY72706
ID AAY72706 standard; protein; 672 AA.
XX AC AAY72706;
XX AC
XX AC
DT 06-AUG-2003 (revised)
DT 31-MAY-2001 (first entry)
XX Parvovirus non-structure protein 1 (NS1) variant (T363A).
XX NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
XX tumoural disease; gene therapy; mutant; mutein; variant.
XX Parvovirus.
XX Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 363
FT /note= "Wild type Thr substituted with Ala"
PN
XX EP1077260-Al.
XX
XX
PD 21-FEB-2001.
XX
PF 13-AUG-1999; 99EP-00115161.
XX
XX 13-AUG-1999; 99EP-00115161.
PR
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Nueesch J, Rommelaere J;
PI
XX WPI; 2001-212717/22.
XX N-PSDB; AAD02801.
DR
XX Novel parvovirus non-structure protein variant, useful for treating
PT tumoral diseases, has a shifted equilibrium between DNA replication and
PT transcription activities, and cytotoxic activity.
XX
XX Claim 6; Page 19-21; 41pp; English.
PS
XX The present sequence is parvovirus non-structure protein 1 (NS1) variant
CC (T363A). The invention relates to the variants of the parvovirus non-
CC structure protein (NS1) having a shifted equilibrium between the DNA
CC replication and transcription activities, and the cytotoxicity activity.
CC These variants are useful as toxins for treating tumoral diseases. The
CC variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
CC 2003 to correct OS field.)
XX
XX Sequence 672 AA;
SQ
Query Match 97.1%; Score 33; DB 4; Length 672;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db 378 CHAIC 382
RESULT 66
AAAY72702
ID AAY72702 standard; protein; 672 AA.
XX
AC AAY72702;
XX
XX 06-AUG-2003 (revised)
DT 31-MAY-2001 (first entry)
XX
XX Parvovirus wild-type non-structure protein 1 (NS1).
DE
XX NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
KW tumoural disease; gene therapy.
XX
XX Parvovirus.
OS
XX EP1077260-Al.
PN
XX 21-FEB-2001.
PD
XX 13-AUG-1999; 99EP-00115161.
PF
XX 13-AUG-1999; 99EP-00115161.
PR
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Nueesch J, Rommelaere J;
PI
XX

DR WPI; 2001-212717/22.
DR N-PSDB; AAD02797.
XX
XX Novel parvovirus non-structure protein variant, useful for treating
PT tumoral diseases, has a shifted equilibrium between DNA replication and
PT transcription activities, and cytotoxic activity.
XX
XX Disclosure; Fig 1; 41pp; English.
PS
XX The present sequence is a parvovirus wild-type non-structure protein 1
CC (NS1). The present invention relates to the variants of the parvovirus
CC non-structure protein (NS1) having a shifted equilibrium between the DNA
CC replication and transcription activities, and the cytotoxicity activity.
CC These variants are useful as toxins for treating tumoural diseases. The
CC variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
CC 2003 to correct OS field.)
XX
XX Sequence 672 AA;
SQ
Query Match 97.1%; Score 33; DB 4; Length 672;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db 378 CHAIC 382
RESULT 67
AAAY72704
ID AAY72704 standard; protein; 672 AA.
XX
AC AAY72704;
XX
XX 06-AUG-2003 (revised)
DT 31-MAY-2001 (first entry)
XX
XX Parvovirus non-structure protein 1 (NS1) variant (S283A).
DE
XX NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
KW tumoural disease; gene therapy; mutant; mutein; variant.
XX
XX Parvovirus.
OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 283
FT /note= "Wild type Ser substituted with Ala"
XX
XX EP1077260-Al.
PN
XX 21-FEB-2001.
PD
XX 13-AUG-1999; 99EP-00115161.
PF
XX 13-AUG-1999; 99EP-00115161.
PR
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Nueesch J, Rommelaere J;
PI
XX WPI; 2001-212717/22.
XX N-PSDB; AAD02799.
DR
XX Novel parvovirus non-structure protein variant, useful for treating
PT tumoral diseases, has a shifted equilibrium between DNA replication and
PT transcription activities, and cytotoxic activity.
XX
XX Claim 6; Page 14-16; 41pp; English.
PS
XX The present sequence is parvovirus non-structure protein 1 (NS1) variant
CC (S283A). The invention relates to the variants of the parvovirus non-
CC structure protein (NS1) having a shifted equilibrium between the DNA

CC replication and transcription activities, and the cytotoxicity activity.
 CC These variants are useful as toxins for treating tumoural diseases. The
 CC variant DNAs are useful as vectors for gene therapy. (Updated on 06-AUG-
 CC 2003 to correct OS field.)
 XX

SQ Sequence 672 AA;

Query Match 97.1%; Score 33; DB 4; Length 672;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||:
 Db 378 CHAIC 382

RESULT 68

ADO34065
 ID ADO34065 standard; peptide; 16 AA.

XX ADO34065;

DT 26-AUG-2004 (first entry)

XX Human CLA2.3 peptide fragment, SEQ ID 28.

DE Cytostatic; human; Colorectal Lesion Associated 2; CLA2; chromosome 5p14;
 KW proliferative disorder; tumour; cancer; carcinoma; dysplasia.

XX Homo sapiens.

XX EPI426442-A1.

XX 09-JUN-2004.

XX 02-DEC-2002; 2002EP-00026772.

XX 02-DEC-2002; 2002EP-00026772.

XX (MTMM-) MTM LAB AG.

XX Hipfel R;

XX WPI; 2004-422595/40.

XX New isolated colorectal lesion associated nucleic acid molecule useful in
 PT the detection and therapy of proliferative disorders.

XX Claim 6; SEQ ID NO 28; 123pp; English.

XX The present invention relates to the human Colorectal Lesion Associated 2
 CC (CLA2) gene (I; ADO34039), which is located on chromosome 5p14. CLA2
 CC sequences are useful for the detection and treatment of proliferative
 CC disorders such as: a benign and malignant tumour (head, neck, respiratory
 CC tract, gastrointestinal tract, skin and its appendages, central and
 CC peripheral nervous system, urinary system, reproductive system, endocrine
 CC system, soft tissues and bone, lymphopoietic and haematopoietic system,
 CC breast, anogenital or colorectal cancers), a carcinoma or a dysplasia.
 CC The present sequence was used to illustrate the invention.

XX Sequence 16 AA;

Query Match 91.2%; Score 31; DB 8; Length 16;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||:
 Db 1 CHALC 5

RESULT 69

AAM15812

ID AAM15812 standard; protein; 20 AA.

XX AAM15812;

DT 12-OCT-2001 (first entry)

XX Peptide #2246 encoded by probe for measuring cervical gene expression.

DE Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

XX Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000670.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 20638; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes
 CC (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||:
 Db 1 CHALC 5

RESULT 70

ABB34809

ID ABB34809 standard; peptide; 20 AA.

XX ABB34809;

XX 04-FEB-2002 (first entry)

XX Peptide #2315 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.
PN
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
PT
XX Claim 27; SEQ ID NO 27444; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: the sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 AA;
SQ

Query Match 91.2%; Score 31; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db |||:|
1 CHALC 5

RESULT 71
AAM28322
ID AAM28322 standard; protein; 20 AA.
XX
XX AAM28322;
AC
XX
XX 17-OCT-2001 (first entry)
DT
XX
XX Peptide #2359 encoded by probe for measuring placental gene expression.
DE
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
KW
XX Homo sapiens.
OS
XX
XX WO200157272-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000663.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR

PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
PT
XX Claim 27; SEQ ID NO 28591; 654pp; English.
PS
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AA1315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
XX Sequence 20 AA;
SQ

Query Match 91.2%; Score 31; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHAVC 5
Db |||:|
1 CHALC 5

RESULT 72
ABB29631
ID ABB29631 standard; peptide; 20 AA.
XX
XX ABB29631;
AC
XX
XX 01-FEB-2002 (first entry)
DT
XX
XX Peptide #2282 encoded by breast cell single exon nucleic acid probe.
DE
XX
XX Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.
KW
XX Homo sapiens.
OS
XX
XX WO200157271-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000662.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
DR
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 12599; 327pp + Sequence Listing; English.
PS
XX The invention relates to a spatially-addressable set of single exon
CC

CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHALC 5
|||:|

RESULT 73

ABB20225
ID ABB20225 standard; protein; 20 AA.

XX
AC ABB20225;

DT 23-JAN-2002 (first entry)

DE Protein #2224 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488999/53.

XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX Claim 15; SEQ ID NO 21995; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHALC 5
|||:|

RESULT 74

AAM67996
ID AAM67996 standard; protein; 20 AA.

XX
AC AAM67996;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28302.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488990/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX Example 4; SEQ ID NO 28302; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention

XX SQ Sequence 20 AA;

Query Match 91.2%; Score 31; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 CHAVC 5
Db      |||:|
        1 CHALC 5

RESULT 75
AAM55611
ID      AAM55611 standard; protein; 20 AA.
XX
AC      AAM55611;
XX
DT      05-NOV-2001 (first entry)
XX
DE      Human brain expressed single exon probe encoded protein SEQ ID NO: 27716.
XX
KW      Human; brain expressed exon; gene expression analysis; probe; microarray;
KW      Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS      Homo sapiens.
XX
PN      WO200157275-A2.
XX
PI      09-AUG-2001.
XX
PF      30-JAN-2001; 2001WO-US000667.
XX
PR      04-FEB-2000; 2000US-0180312P.
PR      26-MAY-2000; 2000US-0207456P.
PR      30-JUN-2000; 2000US-00608408.
PR      03-AUG-2000; 2000US-00632366.
PR      21-SEP-2000; 2000US-0234687P.
PR      27-SEP-2000; 2000US-0236359P.
PR      04-OCT-2000; 2000GB-00024263.
XX
PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PF      WPI; 2001-483446/52.
XX
PR      Single exon nucleic acid probes for analyzing gene expression in human
PR      brains.
XX
PS      Example 4; SEQ ID NO 27716; 650pp + Sequence Listing; English.
XX
CC      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      brain. They can be used to measure gene expression in brain cell samples,
CC      which may enable the diagnosis and improved treatment of nervous system
CC      diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC      epilepsy and cancers. The present sequence is a protein encoded by one of
CC      the probes of the invention
XX
SQ      Sequence 20 AA;
        Query Match          91.2%; Score 31; DB 4; Length 20;
        Best Local Similarity 80.0%; Pred. No. 2.3e+02;
        Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 CHAVC 5
Db      |||:|
        1 CHALC 5

RESULT 76
ABG49637
ID      ABG49637 standard; peptide; 20 AA.
XX
AC      ABG49637;
XX
DT      25-FEB-2003 (first entry)
XX
XX

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```

DE      Human liver peptide, SEQ ID No 28285.
XX
KW      Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW      hypercholesterolaemia; coronary heart disease.
XX
OS      Homo sapiens.
XX
PN      WO200157273-A2.
XX
PD      09-AUG-2001.
XX
PF      30-JAN-2001; 2001WO-US000664.
XX
PR      04-FEB-2000; 2000US-0180312P.
PR      26-MAY-2000; 2000US-0207456P.
PR      30-JUN-2000; 2000US-00608408.
PR      03-AUG-2000; 2000US-00632366.
PR      21-SEP-2000; 2000US-0234687P.
PR      27-SEP-2000; 2000US-0236359P.
PR      04-OCT-2000; 2000GB-00024263.
XX
PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PF      WPI; 2001-488898/53.
XX
PT      Human genome-derived single exon nucleic acid probes useful for analyzing
PT      gene expression in human adult liver.
XX
PS      Claim 27; SEQ ID NO 28285; 658pp; English.
XX
CC      The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC      measuring human gene expression in a sample derived from human adult
CC      liver, comprising one of 13109 defined nucleotide sequences given in the
CC      specification (or complements/ fragments). The probe hybridises at high
CC      stringency to a nucleic acid molecule expressed in the human adult liver.
CC      (I) may be used for predicting, measuring and displaying gene expression
CC      in samples derived from human adult liver. The genes identified may be
CC      involved in genetic liver diseases such as cirrhosis,
CC      hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC      associated with coronary heart disease. ABG47348-ABG59930 represent human
CC      liver single exon encoded peptides of the invention. Note: The sequence
CC      information for this patent does not appear in the printed specification
CC      but was obtained in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 20 AA;
        Query Match          91.2%; Score 31; DB 4; Length 20;
        Best Local Similarity 80.0%; Pred. No. 2.3e+02;
        Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 CHAVC 5
Db      |||:|
        1 CHALC 5

RESULT 77
AAM03550
ID      AAM03550 standard; protein; 20 AA.
XX
AC      AAM03550;
XX
DT      09-OCT-2001 (first entry)
XX
DE      Peptide #2232 encoded by probe for measuring breast gene expression.
XX
KW      Probe; human; breast disease; breast cancer; development disorder;
KW      inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS      Homo sapiens.
XX

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PN WO200157270-A2.
XX
XX
XX 09-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US0000661.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000US-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.
XX
XX Claim 27; SEQ ID NO 12290; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes
XX (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for measuring human gene expression in
XX a human breast sample, where the probe hybridizes at high stringency to a
XX nucleic acid expressed in the human breast. The probes are useful for
XX predicting, diagnosing, grading, staging, monitoring and prognosing
XX diseases of the human breast, particularly those diseases with polygenic
XX aetiology. The diseases include: breast cancer, disorders of development,
XX inflammatory diseases of the breast, fibrocystic changes, proliferative,
XX breast disease and non-carcinoma tumours. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 AA;
XX
XX Query Match 91.2%; Score 31; DB 4; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 2.3e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CHAUC 5
XX Db 1 CHALC 5
XX
XX RESULT 78
XX ABG37528
XX ID ABG37528 standard; peptide; 20 AA.
XX
XX AC ABG37528;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human peptide encoded by genome-derived single exon probe SEQ ID 27193.
XX
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX

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XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US0000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000US-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 27193; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 13614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene,
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 AA;
XX
XX Query Match 91.2%; Score 31; DB 5; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 2.3e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CHAUC 5
XX Db 1 CHALC 5
XX

```


QY 1 CHAVC 5
 ||:|
 Db 44 CHSVC 48

RESULT 81
 ID AAO09658
 AA AAO09658 standard; protein; 61 AA.
 XX
 AC AAO09658;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 XX Human polypeptide SEQ ID NO 23550.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 XX WO200164835-A2.
 PN
 XX
 XX 07-SEP-2001.
 PD
 XX
 XX 26-FEB-2001; 2001WO-US004927.
 PP
 XX
 XX 28-FEB-2000; 2000US-00515126.
 PR
 XX 18-MAY-2000; 2000US-00577409.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-514838/56.
 XX
 XX N-PSDB; AAI89589.
 DR
 XX
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 PT
 XX
 XX Claim 20; SEQ ID NO 23550; 1399pp + Sequence Listing; English.
 PS
 XX
 XX The invention relates to human polynucleotides (AAI79941-AAI93041) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 61 AA;

Query Match 91.2%; Score 31; DB 4; Length 61;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 ||:|
 Db 53 CHSVC 57

RESULT 82
 ID AAY27620
 AA AAY27620 standard; protein; 63 AA.
 XX
 XX AAY27620;
 AC

30-JUL-1999 (first entry)
 Human secreted protein encoded by gene No. 54.

Human; secreted protein; fusion protein; gene therapy; protein therapy;
 diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 developmental abnormality; foetal deficiency; blood; allergy; renal;
 immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;
 inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 XX WO9924836-A1.
 PN
 XX
 XX 20-MAY-1999.
 PD
 XX
 XX 04-NOV-1998; 98WO-US023435.
 PF
 XX
 XX 07-NOV-1997; 97US-0064900P.
 PR
 XX 07-NOV-1997; 97US-0064908P.
 PR
 XX 07-NOV-1997; 97US-0064911P.
 PR
 XX 07-NOV-1997; 97US-0064912P.
 PR
 XX 07-NOV-1997; 97US-0064983P.
 PR
 XX 07-NOV-1997; 97US-0064984P.
 PR
 XX 07-NOV-1997; 97US-0064985P.
 PR
 XX 07-NOV-1997; 97US-0064987P.
 PR
 XX 07-NOV-1997; 97US-0064988P.
 PR
 XX 07-NOV-1997; 97US-0066089P.
 PR
 XX 17-NOV-1997; 97US-0066090P.
 PR
 XX 17-NOV-1997; 97US-0066094P.
 PR
 XX 17-NOV-1997; 97US-0066095P.
 PR
 XX 17-NOV-1997; 97US-0066100P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 XX Feng P, Carter KC, Endress GA, Rosen CA, Ruben SM, Janat F;
 PI Ni J, Wei Y, Moore PA, Soppet DR, Kyaw H, Lafleur DW, Olsen HS;
 PI Shi Y, Ebner R;
 XX
 XX WPI; 1999-337740/28.
 DR
 XX N-PSDB; AAX84986.
 DR
 XX
 XX New human secreted proteins and coding sequences useful for treating
 PT disorders of the immune system and hyperproliferative disorders.
 PT
 XX
 XX Claim 11; Page 381; 507pp; English.

This sequence represents a secreted human protein encoded by the gene
 clone detailed in the descriptor line. The gene can be used to generate
 fusion proteins by linking to the gene to a human immunoglobulin FC
 portion (e.g. AAX84924) for increasing the stability of the fused protein
 as compared to the human protein only. The invention relates to 125 novel
 genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino
 acid sequences AAY27567-Y27933) which are useful for preventing, treating
 or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 125 polynucleotides, based on which tissues they are most highly
 CC expressed in (see AAX84933 for described uses)
 XX
 SQ Sequence 63 AA;

Query Match 91.2%; Score 31; DB 2; Length 63;
 Best Local Similarity 80.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 ||:|

Db 19 CHSVC 23

RESULT 83
AAM15142
ID AAM15142 standard; protein; 63 AA.
XX AAM15142;
AC AAM15142;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #1576 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 19968; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SEN: see AAI10068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENs are derived from human Hela cells. The SENs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 63 AA;
XX
XX Query Match 91.2%; Score 31; DB 4; Length 63;
XX Best Local Similarity 80.0%; Pred. No. 5.9e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CHAVC 5
XX |||||
XX 36 CHALC 40
XX
XX DB
XX
XX RESULT 84
XX ABB34134
XX ID ABB34134 standard; peptide; 63 AA.
XX
XX AC ABB34134;
XX
XX DT 04-FEB-2002 (first entry)
XX
XX 04-FEB-2000; 2000US-0180312P.
XX

DE Peptide #1640 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX Claim 27; SEQ ID NO 26769; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 63 AA;
XX
XX Query Match 91.2%; Score 31; DB 4; Length 63;
XX Best Local Similarity 80.0%; Pred. No. 5.9e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CHAVC 5
XX |||||
XX 36 CHALC 40
XX
XX DB
XX
XX RESULT 85
XX AAM27597
XX ID AAM27597 standard; protein; 63 AA.
XX
XX AC AAM27597;
XX
XX DT 17-OCT-2001 (first entry)
XX
XX DE Peptide #1634 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
XX OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX

PS Claim 15; SEQ ID NO 21345; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see

CC ABA21535-ABA411305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying

CC gene expression in samples derived from the human heart via microarrays.

CC By measuring gene expression, the probes are useful for predicting,

CC diagnosing, grading, staging, monitoring and prognosing diseases of the

CC human heart and vascular system e.g. cardiovascular disease,

CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 63 AA;

Query Match 91.2%; Score 31; DB 4; Length 63;

Best Local Similarity 80.0%; Pred. No. 5.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 36 CHALC 40

RESULT 88

AAM67305

ID AAM67305 standard; protein; 63 AA.

XX

AC AAM67305;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27611.

XX

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX

OS Homo sapiens.

XX

PN WO200157276-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000668.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX

DR WPI; 2001-488900/53.

XX

PT Single exon nucleic acid probes for analyzing gene expression in human brains.

PS Example 4; SEQ ID NO 27611; 658pp + Sequence Listing; English.

XX

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention

XX

SQ Sequence 63 AA;

Query Match 91.2%; Score 31; DB 4; Length 63;

Best Local Similarity 80.0%; Pred. No. 5.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 36 CHALC 40

RESULT 90

ABG48967

ID ABG48967 standard; peptide; 63 AA.

```

KW AC ABG48967;
KW AC
KW DT 25-FEB-2003 (first entry)
KW DE
KW DE Human liver peptide, SEQ ID NO 27615.
KW KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW KW hypercholesterolaemia; coronary heart disease.
KW OS Homo sapiens.
KW PN WO200157273-A2.
KW XX
KW XX 09-AUG-2001.
KW XX 29-JAN-2001; 2001WO-US000661.
KW XX 04-FEB-2000; 2000US-0180312P.
KW PR 26-MAY-2000; 2000US-0207456P.
KW PR 30-JUN-2000; 2000US-00608408.
KW PR 03-AUG-2000; 2000US-00632366.
KW PR 21-SEP-2000; 2000US-0234687P.
KW PR 27-SEP-2000; 2000US-0236359P.
KW PR 04-OCT-2000; 2000GB-00024263.
KW XX (MOLE-) MOLECULAR DYNAMICS INC.
KW PA Penn SG, Hanzel DK, Chen W, Rank DR;
KW PI WPI; 2001-476286/51.
KW XX
KW XX Novel single exon nucleic acid probe used to measuring gene expression in
KW PT a human breast.
KW PS Claim 27; SEQ ID NO 11623; 322pp; English.
KW XX
KW CC The present invention relates to novel single exon nucleic acid probes
KW CC (see AA100010-AA110067). The present sequence is a peptide encoded by one
KW CC such probe. The probes are useful for measuring human gene expression in
KW CC a human breast sample, where the probe hybridises at high stringency to a
KW CC nucleic acid expressed in the human breast. The probes are useful for
KW CC predicting, diagnosing, grading, staging, monitoring and prognosing
KW CC diseases of the human breast, particularly those diseases with polygenic
KW CC aetiology. The diseases include: breast cancer, disorders of development,
KW CC inflammatory diseases of the breast, fibrocystic changes, proliferative
KW CC breast disease and non-carcinoma tumours. Note: The sequence data for
KW CC this patent did not form part of the printed specification, but was
KW CC obtained in electronic format directly from WIPO at
KW CC ftp.wipo.int/pub/published_pct_sequences
KW XX
KW SQ Sequence 63 AA;
KW
KW Query Match 91.2%; Score 31; DB 4; Length 63;
KW Best Local Similarity 80.0%; Pred. No. 5.9e+02;
KW Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
KW
KW QY 1 CHAVC 5
KW DB 36 CHALC 40
KW
KW RESULT 92
KW ABG36952
KW ID ABG36952 standard; peptide; 63 AA.
KW XX
KW AC ABG36952;
KW XX
KW DT 19-AUG-2002 (first entry)
KW XX
KW DE Human peptide encoded by genome-derived single exon probe SEQ ID 26617.
KW XX
KW KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW KW chronic obstructive pulmonary disease; interstitial lung disease;
KW KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW KW primary ciliary dyskinesia; pulmonary hypertension;

```

```

KW AC ABG48967;
KW AC
KW DT 25-FEB-2003 (first entry)
KW DE
KW DE Human liver peptide, SEQ ID NO 27615.
KW KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW KW hypercholesterolaemia; coronary heart disease.
KW OS Homo sapiens.
KW PN WO200157273-A2.
KW XX
KW XX 09-AUG-2001.
KW XX 29-JAN-2001; 2001WO-US000664.
KW XX 04-FEB-2000; 2000US-0180312P.
KW PR 26-MAY-2000; 2000US-0207456P.
KW PR 30-JUN-2000; 2000US-00608408.
KW PR 03-AUG-2000; 2000US-00632366.
KW PR 21-SEP-2000; 2000US-0234687P.
KW PR 27-SEP-2000; 2000US-0236359P.
KW PR 04-OCT-2000; 2000GB-00024263.
KW XX (MOLE-) MOLECULAR DYNAMICS INC.
KW PA Penn SG, Hanzel DK, Chen W, Rank DR;
KW PI WPI; 2001-488898/53.
KW XX
KW XX Human genome-derived single exon nucleic acid probes useful for analyzing
KW PT gene expression in human adult liver.
KW PS Claim 27; SEQ ID NO 27615; 658pp; English.
KW XX
KW CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
KW CC measuring human gene expression in a sample derived from human adult
KW CC liver, comprising one of 13109 defined nucleotide sequences given in the
KW CC specification (or complements/ fragments). The probe hybridises at high
KW CC stringency to a nucleic acid molecule expressed in the human adult liver.
KW CC (I) may be used for predicting, measuring and displaying gene expression
KW CC in samples derived from human adult liver. The genes identified may be
KW CC involved in genetic liver diseases such as cirrhosis.
KW CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
KW CC associated with coronary heart disease. ABG47348-ABG59930 represent human
KW CC liver single exon encoded peptides of the invention. Note: The sequence
KW CC information for this patent does not appear in the printed specification
KW CC but was obtained in electronic format directly from WIPO at
KW CC ftp.wipo.int/pub/published_pct_sequences
KW XX
KW SQ Sequence 63 AA;
KW
KW Query Match 91.2%; Score 31; DB 4; Length 63;
KW Best Local Similarity 80.0%; Pred. No. 5.9e+02;
KW Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
KW
KW QY 1 CHAVC 5
KW DB 36 CHALC 40
KW
KW RESULT 91
KW AAM02883
KW ID AAM02883 standard; protein; 63 AA.
KW XX
KW AC AAM02883;
KW XX
KW DT 09-OCT-2001 (first entry)
KW XX
KW DE Peptide #1565 encoded by probe for measuring breast gene expression.

```

KW hyaline membrane disease.
XX Homo sapiens.
OS WO200186003-A2.
PN 15-NOV-2001.
XX 30-JAN-2001; 2001WO-US000665.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX Claim 27; SEQ ID NO 26617; 634pp; English.
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 63 AA;
XX Query Match 91.2%; Score 31; DB 5; Length 63;
XX Best Local Similarity 80.0%; Pred. No. 5.9e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

KW 1 CHAVC 5
XX |||:|
Db 36 CHALC 40
RESULT 93
AAM24070
ID AAM24070 standard; protein; 85 AA.
XX AAM24070;
XX 12-OCT-2001 (first entry)
XX Human EST encoded protein SEQ ID NO: 1595.
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX Homo sapiens.
OS WO200154477-A2.
PN 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US002687.
XX 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00638870.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
DR N-PSDB; AAH98729.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX Claim 20; Page 1089; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX Sequence 85 AA;
XX Query Match 91.2%; Score 31; DB 4; Length 85;
XX Best Local Similarity 80.0%; Pred. No. 7.7e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

KW 1 CHAVC 5
XX |||:|
Db 78 CHALC 82
RESULT 94
AAU14419
ID AAU14419 standard; protein; 96 AA.
XX AAU14419;
XX


```
Db      81 CHSVC 85
||:|
RESULT 96
ADO34044
ID ADO34044 standard; protein; 100 AA.
XX
AC ADO34044;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human CLA2.3, SEQ ID 7.
XX
KW Cytostatic; human; Colorectal Lesion Associated 2; CLA2; chromosome 5p14;
KW proliferative disorder; tumour; cancer; carcinoma; dysplasia.
XX
OS Homo sapiens.
XX
PN EPI426442-A1.
XX
PD 09-JUN-2004.
XX
PF 02-DEC-2002; 2002EP-00026772.
XX
PR 02-DEC-2002; 2002EP-00026772.
XX
PA (MTMM-) MTM LAB AG.
XX
PI Hipfel R;
XX
DR WPI; 2004-422595/40.
DR N-PSDB; ADO34043.
XX
PT New isolated colorectal lesion associated nucleic acid molecule useful in
PT the detection and therapy of proliferative disorders.
XX
PS Claim 6; SEQ ID NO 7; 123pp; English.
XX
CC The present invention relates to the human Colorectal Lesion Associated 2
CC (CLA2) gene (I; ADO34038), which is located on chromosome 5p14. CLA2
CC sequences are useful for the detection and treatment of proliferative
CC disorders such as: a benign and malignant tumour (head, neck, respiratory
CC tract, gastrointestinal tract, skin and its appendages, central and
CC peripheral nervous system, urinary system, reproductive system, endocrine
CC system, soft tissues and bone, lymphopoietic and haematopoietic system,
CC breast, anogenital or colorectal cancers), a carcinoma or a dysplasia.
CC The present sequence was used to illustrate the invention.
XX
SQ Sequence 100 AA;

Query Match      91.2%; Score 31; DB 8; Length 100;
Best Local Similarity 80.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||:|
Db      85 CHALC 89

RESULT 97
ADM05223
ID ADM05223 standard; protein; 117 AA.
XX
AC ADM05223;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:3908.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.

XX PN EPI347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM02780.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 3908; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 117 AA;

Query Match      91.2%; Score 31; DB 7; Length 117;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||:|
Db      74 CHALC 78

RESULT 98
ABG05990
ID ABG05990 standard; protein; 134 AA.
XX
AC ABG05990;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #5981.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
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```
XX WPI; 2001-639362/73.
DR N-PSDB; RAS70177.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
FT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 36349; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: the sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 134 AA;
SQ
Query Match 91.2%; Score 31; DB 4; Length 134;
Best Local Similarity 80.0%; Pred. NO. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAUC 5
Db 90 CHALC 94
RESULT 99
ADM26297
ID ADM26297 standard; protein; 139 AA.
XX
AC ADM26297;
XX
XX 20-MAY-2004 (first entry)
XX
DE Hyperthermophile Methanopyrus kandleri protein #903.
XX
KW hyperthermophile; protein stability enhancement;
KW protein activity enhancement.
XX
OS Methanopyrus kandleri.
XX
PN WO2003076575-A2.
XX
PD 18-SEP-2003.
XX
PF 04-MAR-2003; 2003WO-US006664.
XX
PR 04-MAR-2002; 2002US-0361742P.
PR 14-MAY-2002; 2002US-0380423P.
PR 16-SEP-2002; 2002US-0410974P.
XX
XX (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
XX
XX Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;
PI
```

```
XX WPI; 2003-748383/70.
DR N-PSDB; ADM27081.
XX
PT New isolated nucleic acids encoding any of about 1700 Methanopyrus
FT kandleri proteins, and the encoded proteins, useful as a medicaments or
PT as diagnostic agents.
XX
PS Claim 31; SEQ ID NO 903; 1023pp; English.
XX
CC The invention comprises the amino acid sequence of proteins from the
CC hyperthermophile Methanopyrus kandleri, the invention also comprises the
CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri
CC proteins of the invention are useful for enhancing the stability and/or
CC activity of other proteins. The Methanopyrus kandleri genome is useful in
CC a variety of diagnostic and analytical methods. The present amino acid
CC sequence represents a Methanopyrus kandleri protein of the invention.
XX
XX Sequence 139 AA;
SQ
Query Match 91.2%; Score 31; DB 7; Length 139;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAUC 5
Db 91 CHSVC 95
RESULT 100
ABJ18656
ID ABJ18656 standard; protein; 148 AA.
XX
AC ABJ18656;
XX
XX 20-FEB-2003 (first entry)
XX
DE Human erbB receptor subdomain IV protein #1.
XX
KW Human; vaccine; erbB receptor antagonist; tumour; cancer; gastric cancer;
KW breast cancer; prostate cancer; erbB receptor subdomain IV.
XX
OS Homo sapiens.
XX
PN WO200281649-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US011211.
XX
PR 06-APR-2001; 2001US-0282037P.
PR 03-AUG-2001; 2001US-0309864P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
PI Greene MI, Zhang H, Murali R, Richter M, Berezov A, Liu Q;
PI Chen J;
XX
XX WPI; 2003-075482/07.
XX
XX New peptide antagonists against erbB receptors, useful for preventing or
XX treating tumors or cancers (e.g. lung adenocarcinomas, breast carcinomas
XX or prostate cancer) in humans.
XX
PS Claim 46; Page 110-111; 115pp; English.
XX
CC The invention comprises peptide antagonists designed to target erbB
CC receptors. The erbB receptor peptide antagonists are useful for
CC preventing tumours and cancers (e.g. gastric cancer, breast cancer and
CC prostate cancer). The present amino acid sequence represents a human erbB
CC subdomain IV protein
XX
XX Sequence 148 AA;
SQ
```

Query Match 91.2%; Score 31; DB 6; Length 148;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 3 CHALC 7

Search completed: July 26, 2005, 23:58:04
Job time : 168 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 23:52:35 ; Search time 41 Seconds
(without alignments)

9.104 Million cell updates/sec

Title: US-10-632-678-10

Perfect score: 34

Sequence: 1 CHAVC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	34	100.0	5	3	US-08-996-679-8
3	34	100.0	5	3	US-09-115-395-10
4	34	100.0	5	3	US-09-102-540-15175
5	34	100.0	5	3	US-09-507-102-8
6	34	100.0	5	3	US-09-250-059-10
7	34	100.0	5	3	US-09-248-074-11
8	34	100.0	5	4	US-09-458-870-10
9	34	100.0	5	4	US-09-057-363C-22
10	34	100.0	5	4	US-09-057-363C-22
11	34	100.0	5	4	US-09-248-015-10
12	34	100.0	5	4	US-09-544-782-10
13	34	100.0	5	4	US-09-234-395-296
14	34	100.0	5	4	US-09-305-928-236
15	34	100.0	5	4	US-09-265-107-22
16	34	100.0	5	4	US-09-265-107-34
17	34	100.0	5	4	US-10-058-821-10
18	34	100.0	6	4	US-09-458-870-84
19	34	100.0	6	4	US-09-458-870-87
20	34	100.0	6	4	US-09-458-870-88
21	34	100.0	6	4	US-09-458-870-91
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23	34	100.0	6	4	US-09-458-870-93
24	34	100.0	6	4	US-09-458-870-100
25	34	100.0	6	4	US-09-544-782-54
26	34	100.0	6	4	US-09-544-782-84
27	34	100.0	6	4	US-09-544-782-87

28	34	100.0	6	4	US-09-544-782-88	Sequence 88, Appl
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31	34	100.0	6	4	US-09-544-782-93	Sequence 93, Appl
32	34	100.0	7	4	US-09-458-870-89	Sequence 89, Appl
33	34	100.0	7	4	US-09-458-870-90	Sequence 90, Appl
34	34	100.0	7	4	US-09-458-870-96	Sequence 96, Appl
35	34	100.0	7	4	US-09-544-782-89	Sequence 89, Appl
36	34	100.0	7	4	US-09-544-782-90	Sequence 90, Appl
37	34	100.0	7	4	US-09-544-782-96	Sequence 96, Appl
38	34	100.0	8	4	US-09-458-870-95	Sequence 95, Appl
39	34	100.0	8	4	US-09-458-870-101	Sequence 101, Appl
40	34	100.0	8	4	US-09-544-782-95	Sequence 95, Appl
41	34	100.0	542	4	US-08-311-731A-213	Sequence 213, App
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43	31	91.2	257	4	US-09-543-681A-7794	Sequence 7794, Ap
44	31	91.2	312	3	US-09-210-637-34	Sequence 34, Appl
45	31	91.2	313	3	US-09-347-878-30	Sequence 30, Appl
46	31	91.2	313	4	US-09-367-007C-39	Sequence 39, Appl
47	31	91.2	339	4	US-09-949-016-10160	Sequence 10160, A
48	31	91.2	644	1	US-08-336-708A-9	Sequence 9, Appl
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50	31	91.2	1210	2	US-08-484-438-7	Sequence 7, Appl
51	31	91.2	1210	2	US-08-475-035-4	Sequence 4, Appl
52	31	91.2	1210	4	US-09-715-249-2	Sequence 2, Appl
53	30	88.2	5	3	US-08-893-534A-9	Sequence 9, Appl
54	30	88.2	5	3	US-08-996-679-9	Sequence 9, Appl
55	30	88.2	5	3	US-09-115-395-20	Sequence 20, Appl
56	30	88.2	5	3	US-09-507-102-9	Sequence 9, Appl
57	30	88.2	5	3	US-09-250-059-11	Sequence 11, Appl
58	30	88.2	5	3	US-09-248-074-11	Sequence 11, Appl
59	30	88.2	5	4	US-09-357-717-11	Sequence 11, Appl
60	30	88.2	5	4	US-09-458-870-11	Sequence 11, Appl
61	30	88.2	5	4	US-09-248-015-20	Sequence 20, Appl
62	30	88.2	5	4	US-08-544-782-11	Sequence 11, Appl
63	30	88.2	5	4	US-10-058-821-11	Sequence 11, Appl
64	30	88.2	16	4	US-09-910-009A-358	Sequence 358, App
65	30	88.2	16	4	US-09-910-009A-454	Sequence 454, App
66	30	88.2	17	3	US-08-331-625A-35	Sequence 35, Appl
67	30	88.2	17	3	US-09-494-151-35	Sequence 35, Appl
68	30	88.2	17	4	US-09-972-484-35	Sequence 35, Appl
69	30	88.2	65	4	US-09-910-009A-357	Sequence 357, App
70	30	88.2	145	4	US-09-328-352-7139	Sequence 7139, Ap
71	30	88.2	165	4	US-09-270-767-39899	Sequence 39899, A
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73	30	88.2	203	3	US-08-331-625A-11	Sequence 11, Appl
74	30	88.2	203	3	US-08-494-151-11	Sequence 11, Appl
75	30	88.2	203	4	US-09-972-484-11	Sequence 11, Appl
76	30	88.2	234	4	US-09-902-540-15175	Sequence 15175, A
77	30	88.2	301	4	US-09-489-039A-9117	Sequence 9117, Ap
78	30	88.2	342	4	US-09-244-805-62	Sequence 62, Appl
79	30	88.2	374	2	US-07-857-224B-85	Sequence 85, Appl
80	30	88.2	525	4	US-09-902-540-10986	Sequence 10986, A
81	30	88.2	777	4	US-09-270-767-44409	Sequence 44409, A
82	30	88.2	1101	3	US-08-331-625A-52	Sequence 52, Appl
83	30	88.2	1101	3	US-09-494-151-52	Sequence 52, Appl
84	30	88.2	1101	4	US-09-972-484-52	Sequence 52, Appl
85	30	88.2	1401	1	US-08-308-872B-2	Sequence 2, Appl
86	30	88.2	1451	1	US-08-308-872B-4	Sequence 4, Appl
87	30	88.2	1452	3	US-08-331-625A-2	Sequence 2, Appl
88	30	88.2	1452	3	US-09-494-151-2	Sequence 2, Appl
89	30	88.2	1452	4	US-09-972-484-2	Sequence 2, Appl
90	30	88.2	1452	5	PCT-US93-04384-18	Sequence 18, Appl
91	30	88.2	1452	5	PCT-US93-04692-2	Sequence 2, Appl
92	30	88.2	1454	3	US-08-392-459-22	Sequence 22, Appl
93	30	88.2	1454	3	US-08-392-459-26	Sequence 26, Appl
94	30	88.2	1454	4	US-09-854-799-22	Sequence 22, Appl
95	30	88.2	1454	4	US-09-854-799-26	Sequence 26, Appl
96	30	88.2	1454	5	PCT-US91-08525-22	Sequence 22, Appl
97	30	88.2	1454	5	PCT-US91-08525-26	Sequence 26, Appl
98	30	88.2	1454	5	PCT-US93-04384-2	Sequence 2, Appl
99	30	88.2	1454	5	PCT-US93-04384-8	Sequence 8, Appl
100	30	88.2	1454	5	PCT-US93-04384-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-893-534A-8
; Sequence 8, Application US/08893534A
; Patent No. 6031072
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,534A
; FILING DATE: 11-JUL-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-893-534A-8

Query Match 100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 2
US-08-996-679-8
; Sequence 8, Application US/08996679
; Patent No. 6169071
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

Query Match 100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,679
; FILING DATE: 23-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-996-679-8

Query Match 100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 3
US-09-115-395-10
; Sequence 10, Application US/09115395A
; Patent No. 6207639
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C3
; CURRENT APPLICATION NUMBER: US/09/115,395A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 08/996,679
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/893,534
; EARLIER FILING DATE: 1997-07-11
; EARLIER APPLICATION NUMBER: 60/021,612
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-115-395-10

Query Match 100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 4
US-09-507-102-8

; Sequence 8, Application US/09507102
; Patent No. 6326352
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; CELL ADHESION
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SED IP LAW GROUP PLLC
; STREET: 6300 Bank of America Bldg., 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,102
; FILING DATE: 17-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/893,534
; FILING DATE: 11-JUL-1997
; APPLICATION NUMBER: US 60/021,612
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 100086.401C10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-507-102-8
Query Match 100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT 5
US-09-250-059-10
; Sequence 10, Application US/09250059
; Patent No. 6333307
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C6
; CURRENT APPLICATION NUMBER: US/09/250,059
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-250-059-10
Query Match 100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT 6
US-09-248-074-10
; Sequence 10, Application US/09248074
; Patent No. 6346512
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C5
; CURRENT APPLICATION NUMBER: US/09/248,074
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-248-074-10
Query Match 100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT 7
US-09-357-717-10
; Sequence 10, Application US/09357717
; Patent No. 6417325
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
; FILE REFERENCE: 100086.401C7
; CURRENT APPLICATION NUMBER: US/09/357,717
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-357-717-10

Query Match          100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
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Db      1 CHAVC 5

RESULT 8
US-09-458-870-10
; Sequence 10, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-10

Query Match          100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
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Db      1 CHAVC 5

RESULT 9
US-09-057-363C-22
; Sequence 22, Application US/09057363C
; Patent No. 6551994
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
; INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,363C
; FILING DATE: 08-Apr-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 100086.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-057-363C-22

Query Match          100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
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Db      1 CHAVC 5

RESULT 10
US-09-057-363C-34
; Sequence 34, Application US/09057363C
; Patent No. 6551994
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
; INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,363C
; FILING DATE: 08-Apr-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 100086.406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: circular
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; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-057-363C-34
Query Match      100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
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RESULT 11
US-09-248-015-10
; Sequence 10, Application US/09248015
; Patent No. 6562786
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS
; FILE REFERENCE: 100086.401C4
; CURRENT APPLICATION NUMBER: US/09/248.015
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-248-015-10
Query Match      100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
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RESULT 12
US-09-544-782-10
; Sequence 10, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544.782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-10
Query Match      100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
      |||||

RESULT 13
US-09-234-395-296
; Sequence 296, Application US/09234395
; Patent No. 6680175
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C2
; CURRENT APPLICATION NUMBER: US/09/234.395
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-296
Query Match      100.0%; Score 34; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1 CHAVC 5
      |||||

RESULT 14
US-09-305-928-296
; Sequence 296, Application US/09305928
; Patent No. 6682901
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C4
; CURRENT APPLICATION NUMBER: US/09/305.928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-296
```



```
RESULT 19
US-09-458-870-87
; Sequence 87, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-87
Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 20
US-09-458-870-88
; Sequence 88, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-88
Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 21
US-09-458-870-91
; Sequence 91, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-91
Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 22
US-09-458-870-92
; Sequence 92, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-92
Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5
```

```

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 23
US-09-458-870-93
; Sequence 93, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-93

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 24
US-09-458-870-100
; Sequence 100, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-100

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 25
US-09-544-782-54
; Sequence 54, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-54

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      2 CHAVC 6

RESULT 26
US-09-544-782-84
; Sequence 84, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-84

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      2 CHAVC 6
```

Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 1 CHAVC 5

RESULT 27
US-09-544-782-87
; Sequence 87, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-87

Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 1 CHAVC 5

RESULT 28
US-09-544-782-88
; Sequence 88, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group

US-09-544-782-88

Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 2 CHAVC 6

RESULT 29
US-09-544-782-91
; Sequence 91, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-91

Query Match 100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 1 CHAVC 5

RESULT 30
US-09-544-782-92
; Sequence 92, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or

```
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-92

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 31
US-09-544-782-93
; Sequence 93, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-93

Query Match      100.0%; Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 32
US-09-458-870-89
; Sequence 89, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-89

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      2 CHAVC 6

RESULT 33
US-09-458-870-90
; Sequence 90, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-90

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
      |||||
Db      2 CHAVC 6

RESULT 34
US-09-458-870-96
; Sequence 96, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
```

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-96

Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 3 CHAVC 7

RESULT 35
US-09-544-782-89
; Sequence 89, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-89

Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 1 CHAVC 5

RESULT 36
US-09-544-782-90
; Sequence 90, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-90

Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 2 CHAVC 6

RESULT 37
US-09-544-782-96
; Sequence 96, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-96

Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
Db 3 CHAVC 7

RESULT 38
US-09-458-870-95
; Sequence 95, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 8
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-95

Query Match 100.0%; Score 34; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 3 CHAVC 7

RESULT 39

US-09-458-870-101
; Sequence 101, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)
; OTHER INFORMATION: Where Xaa is beta,beta-dimethyl cysteine
US-09-458-870-101

Query Match 100.0%; Score 34; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 3 CHAVC 7

RESULT 40

US-09-544-782-95
; Sequence 95, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9

; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-95

Query Match 100.0%; Score 34; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 3 CHAVC 7

RESULT 41

US-08-311-731A-213
; Sequence 213, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-213

Query Match 100.0%; Score 34; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 1 CHAVC 5

RESULT 42
US-09-949-016-10680
; Sequence 10680, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10680
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10680

Query Match 97.1%; Score 33; DB 4; Length 163;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 65 CHAIC 69

RESULT 43
US-09-543-681A-7794
; Sequence 7794, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7794
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7794

Query Match 91.2%; Score 31; DB 4; Length 257;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 32 CHAIC 36

RESULT 44
US-09-230-637-34
; Sequence 34, Application US/09230637
```

```
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-230-637-34

Query Match 91.2%; Score 31; DB 3; Length 312;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 194 CHAIC 198

RESULT 45
US-09-347-878-30
; Sequence 30, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human thymidylate synthase protein sequence
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: D00596/GenBank
US-09-347-878-30

Query Match 91.2%; Score 31; DB 3; Length 313;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
   |||||
Db 195 CHAIC 199

RESULT 46
US-09-367-007C-39
; Sequence 39, Application US/09367007C
; Patent No. 6416987
; GENERAL INFORMATION:
; APPLICANT: Bertino, Joseph R.
; APPLICANT: Banerjee, Debabrata
; APPLICANT: Tong, Youzhi
; APPLICANT: Liu-Chen, Xinyue
; TITLE OF INVENTION: Mutants of Thymidylate Synthase and Uses Thereof
```

; FILE REFERENCE: D5978
; CURRENT APPLICATION NUMBER: US/09/367,007C
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/US98/02145
; PRIOR FILING DATE: 1998-01-03
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 39
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Wild type human thymidylate synthase amino acid
; OTHER INFORMATION: sequence (Genbank Accession number NP001062)
US-09-367-007C-39

Query Match 91.2%; Score 31; DB 4; Length 313;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 195 CHALC 199

RESULT 47
US-09-949-016-10160
; Sequence 10160, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10160
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10160

Query Match 91.2%; Score 31; DB 4; Length 339;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 221 CHALC 225

RESULT 48
US-08-336-708A-9
; Sequence 9, Application US/08336708A
; Patent No. 5521295
; GENERAL INFORMATION:
; APPLICANT: Pacifici, Robert E.
; APPLICANT: Thomason, Arlen R.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Hybrid Receptor Molecules
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California

; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,708A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy
; REFERENCE/DOCKET NUMBER: A-241A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 644 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-708A-9

Query Match 91.2%; Score 31; DB 1; Length 644;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 506 CHALC 510

RESULT 49
US-09-328-352-7293
; Sequence 7293, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7293
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7293

Query Match 91.2%; Score 31; DB 4; Length 760;
Best Local Similarity 80.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 3 CHALC 7

RESULT 50
US-08-484-438-7
; Sequence 7, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegall, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,438
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/323,442
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: US 08/150,704
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/981,165
; FILING DATE: 24-NOV-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-08-484-438-7

Query Match 91.2%; Score 31; DB 2; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 506 CHALC 510

RESULT 51
US-08-475-035-4
; Sequence 4, Application US/08475035
; Patent No. 5985553
; GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Peirymann, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.656
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-035-4

Query Match 91.2%; Score 31; DB 2; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 506 CHALC 510

RESULT 52
US-09-715-249-2
; Sequence 2, Application US/09715249
; Patent No. 6790614
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; APPLICANT: VERES, GABOR
; APPLICANT: PIPPIG, SUSANNE
; TITLE OF INVENTION: selectable cell surface marker genes
; FILE REFERENCE: 4-31192
; CURRENT APPLICATION NUMBER: US/09/715,249
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: us 60/166594
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: us 09/539248
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: EGFR
; US-09-715-249-2

Query Match 91.2%; Score 31; DB 4; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 506 CHALC 510

RESULT 53
US-08-893-534A-9
; Sequence 9, Application US/08893534A
; Patent No. 6031072
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,679
; FILING DATE: 23-DEC-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-996-679-9

Query Match 88.2%; Score 30; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1 CHGVC 5

RESULT 54
US-08-996-679-9
; Sequence 9, Application US/08996679
; Patent No. 6163071
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,679
; FILING DATE: 23-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-996-679-9

Query Match 88.2%; Score 30; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1 CHGVC 5

RESULT 55
US-09-115-395-20
; Sequence 20, Application US/09115395A
; Patent No. 6207639
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C3
; CURRENT APPLICATION NUMBER: US/09/115.395A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 08/996,679
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/893,534
; EARLIER FILING DATE: 1997-07-11
; EARLIER APPLICATION NUMBER: 60/021,612
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-115-395-20

Query Match 88.2%; Score 30; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1 CHGVC 5

RESULT 56
US-09-507-102-9
; Sequence 9, Application US/09507102
; Patent No. 6326352
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED IP LAW GROUP PLLC
; STREET: 6300 Bank of America Bldg., 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/507,102
FILING DATE: 17-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,534
FILING DATE: 11-JUL-1997
APPLICATION NUMBER: US 60/021,612
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.401C10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: circular
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-507-102-9

Query Match 88.2%; Score 30; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1 CHGVC 5

RESULT 57
US-09-250-059-11
; Sequence 11, Application US/09250059
; Patent No. 6333307
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C6
; CURRENT APPLICATION NUMBER: US/09/250,059
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: control peptide
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-250-059-11

Query Match 88.2%; Score 30; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||

Db 1 CHGVC 5
RESULT 58
US-09-248-074-11
; Sequence 11, Application US/09248074
; Patent No. 6346512
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C5
; CURRENT APPLICATION NUMBER: US/09/248,074
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: control peptide
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-248-074-11

Query Match 88.2%; Score 30; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1 CHGVC 5

RESULT 59
US-09-357-717-11
; Sequence 11, Application US/09357717
; Patent No. 6417325
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
; FILE REFERENCE: 100086.401C7
; CURRENT APPLICATION NUMBER: US/09/357,717
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: control peptide
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-357-717-11

Query Match 88.2%; Score 30; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||

Db 1 CHGVC 5

RESULT 60

US-09-458-870-11
; Sequence 11, Application US/09458870
; Patent No. 6465427
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C8
; CURRENT APPLICATION NUMBER: US/09/458,870
; CURRENT FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: control peptide
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-458-870-11

Query Match 88.2%; Score 30; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
Db 1 CHGVC 5

RESULT 61

US-09-248-015-20
; Sequence 20, Application US/09248015
; Patent No. 6562786
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS
; FILE REFERENCE: 100086.401C4
; CURRENT APPLICATION NUMBER: US/09/248,015
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: control peptide
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-248-015-20

Query Match 88.2%; Score 30; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db |||
1 CHGVC 5

RESULT 62

US-09-544-782-11
; Sequence 11, Application US/09544782
; Patent No. 6610821
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Ammar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C9
; CURRENT APPLICATION NUMBER: US/09/544,782
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: control peptide
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-544-782-11

Query Match 88.2%; Score 30; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
Db 1 CHGVC 5

RESULT 63

US-10-058-821-11
; Sequence 11, Application US/10058821
; Patent No. 6780845
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY
; FILE REFERENCE: 100086.401C12
; CURRENT APPLICATION NUMBER: US/10/058,821
; CURRENT FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic
; OTHER INFORMATION: control peptide
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-058-821-11

Query Match 88.2%; Score 30; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

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Db          1 CHGVC 5
|| ||
; TITLE OF INVENTION: Mu-Conopeptides
; FILE REFERENCE: 2314-242
; CURRENT APPLICATION NUMBER: US/09/910,009A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,619
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/245,157
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/264,319
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/277,270
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 454
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus aulicus
; US-09-910-009A-454

Query Match      88.2%; Score 30; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      7 CHSIC 11

RESULT 64
US-09-910-009A-358
; Sequence 358, Application US/09910009A
; Patent No. 6727226
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Shen, Greg S.
; APPLICANT: Wagstaff, John D.
; TITLE OF INVENTION: Mu-Conopeptides
; FILE REFERENCE: 2314-242
; CURRENT APPLICATION NUMBER: US/09/910,009A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,619
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/245,157
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/264,319
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/277,270
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 358
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus aulicus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Xaa at residue 5 and 6 is Pro or Hyp
US-09-910-009A-358

Query Match      88.2%; Score 30; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      7 CHSIC 11

RESULT 65
US-09-910-009A-454
; Sequence 454, Application US/09910009A
; Patent No. 6727226
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Shen, Greg S.
; APPLICANT: Wagstaff, John D.
```

; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-331-625A-35

Query Match 88.2%; Score 30; DB 3; Length 17;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 8 CHSIC 12

RESULT 67

US-09-494-151-35
; Sequence 35, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Klepfer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-494-151-35

Query Match 88.2%; Score 30; DB 3; Length 17;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 8 CHSIC 12

RESULT 68

US-09-972-484-35
; Sequence 35, Application US/09972484
; Patent No. 6602504
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Klepfer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,484
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-972-484-35

Query Match 88.2%; Score 30; DB 4; Length 17;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 8 CHSIC 12

RESULT 69

US-09-910-009A-357
; Sequence 357, Application US/09910009A
; Patent No. 6727226

; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Shen, Greg S.
; APPLICANT: Wagstaff, John D.
; TITLE OF INVENTION: Mu-Conopeptides
; FILE REFERENCE: 2314-242
; CURRENT APPLICATION NUMBER: US/09/910,009A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,619
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/245,157
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/264,319
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/277,270
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 357
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Conus aulicus
US-09-910-009A-357

Query Match 88.2%; Score 30; DB 4; Length 65;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||:|
Db 55 CHSIC 59

RESULT 70
US-09-328-352-7139
; Sequence 7139, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7139
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7139

Query Match 88.2%; Score 30; DB 4; Length 145;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||:|
Db 13 CHSIC 17

RESULT 71
US-09-270-767-39899
; Sequence 39899, Application US/09270767

; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39899
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39899

Query Match 88.2%; Score 30; DB 4; Length 165;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||:|
Db 107 CHVC 111

RESULT 72
US-09-270-767-55116
; Sequence 55116, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55116
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55116

Query Match 88.2%; Score 30; DB 4; Length 165;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||:|
Db 107 CHVC 111

RESULT 73
US-08-331-625A-11
; Sequence 11, Application US/08331625A
; Patent No. 6057436
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA

```
;
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,625A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,194
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; US-08-331-625A-11
;
; Query Match 88.2%; Score 30; DB 3; Length 203;
; Best Local Similarity 60.0%; Pred. No. 4e+02;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CHAVC 5
; DB 182 CHSIC 186
;
; RESULT 74
; US-09-494-151-11
; Sequence 11, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Kieffer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
;
; Query Match 88.2%; Score 30; DB 3; Length 203;
; Best Local Similarity 60.0%; Pred. No. 4e+02;
; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CHAVC 5
; DB 182 CHSIC 186
;
; RESULT 75
; US-09-972-484-11
; Sequence 11, Application US/09972484
; Patent No. 6602504
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Kieffer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,484
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,484
; FILING DATE: 28-Jan-2000
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
;
```


; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-972-484-11

Query Match 88.2%; Score 30; DB 4; Length 203;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 182 CHSIC 186

RESULT 76
US-09-902-540-15175
; Sequence 15175, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15175
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15175

Query Match 88.2%; Score 30; DB 4; Length 234;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 215 CHATC 219

RESULT 77
US-09-489-039A-9117
; Sequence 9117, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9117
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9117

Query Match 88.2%; Score 30; DB 4; Length 301;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 36 CHAAC 40

RESULT 78
US-09-244-805-62
; Sequence 62, Application US/09244805
; Patent No. 6699660
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/09/244,805
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-805-62

Query Match 88.2%; Score 30; DB 4; Length 342;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 141 CHVC 145

RESULT 79
US-07-857-224B-85
; Sequence 85, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: mouse
; FEATURE: Alcohol dehydrogenase, Table 3 Column 6
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Joernvall, H.
; AUTHORS: Persson, M.
; AUTHORS: Jeffery, J.
; TITLE: Alcohol dehydrogenases
; JOURNAL: Proceedings of the National Academy of Sciences, USA
; VOLUME: 78
; PAGES: 4226-4230
; DATE: 1981
; US-07-857-224B-85

Query Match      88.2%; Score 30; DB 2; Length 374;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
DB      282 CHAAC 286

RESULT 80
US-09-902-540-10986
; Sequence 10986, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10986
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-10986

Query Match      88.2%; Score 30; DB 4; Length 525;
Best Local Similarity 80.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
DB      206 CHVVC 210

RESULT 81
US-09-270-767-44409
; Sequence 44409, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44409
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-44409

Query Match      88.2%; Score 30; DB 4; Length 777;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5
DB      215 CHAAC 219

RESULT 82
US-08-331-625A-52
; Sequence 52, Application US/08331625A
; Patent No. 6057436
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation - Corporate
; ADDRESS: Patente
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,625A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,194
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1101 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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US-08-331-625A-52

Query Match 88.2%; Score 30; DB 3; Length 1101;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1080 CHSIC 1084

RESULT 83

US-09-494-151-52
; Sequence 52, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Klepfer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US/07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1101 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Query Match 88.2%; Score 30; DB 3; Length 1101;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1080 CHSIC 1084

RESULT 84

US-09-972-484-52

; Sequence 52, Application US/09972484
; Patent No. 6602504
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Klepfer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,484
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US/07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1101 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Query Match 88.2%; Score 30; DB 4; Length 1101;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 1080 CHSIC 1084

RESULT 85

US-08-308-872B-2
; Sequence 2, Application US/08308872B
; Patent No. 5661006
; GENERAL INFORMATION:
; APPLICANT: BROWN, Thomas David Kay
; APPLICANT: HORSBURGH, Brian Colin
; TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5661006el Patent Department

```
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,872B
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,846
; FILING DATE: 05-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,641
; FILING DATE: 24-APR-1992
; APPLICATION NUMBER: EP 91.303.737.0
; FILING DATE: 25-APR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1443 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Canina corona virus
; STRAIN: CCV-6
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1443
; OTHER INFORMATION: /label= CCV6_Spike
;
US-08-308-872B-2

Query Match      88.2%; Score 30; DB 1; Length 1443;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1422 CHSIC 1426

RESULT 86
US-08-308-872B-4
; Sequence 4, Application US/08308872B
; Patent No. 5661006
; GENERAL INFORMATION:
; APPLICANT: BROWN, Thomas David Kay
; APPLICANT: HORSBURGH, Brian Colin
; TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5661006el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,872B
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,846
; FILING DATE: 05-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,641
; FILING DATE: 24-APR-1992
; APPLICATION NUMBER: EP 91.303.737.0
; FILING DATE: 25-APR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1443 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Canina corona virus
; STRAIN: CCV-6
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1443
; OTHER INFORMATION: /label= CCV6_Spike
;
US-08-308-872B-2
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,872B
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,846
; FILING DATE: 05-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,641
; FILING DATE: 24-APR-1992
; APPLICATION NUMBER: EP 91.303.737.0
; FILING DATE: 25-APR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1451 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Canine corona virus
; STRAIN: CCVinsAVC-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1451
; OTHER INFORMATION: /label= CCVinsAVC-1_Spike
;
US-08-308-872B-4

Query Match      88.2%; Score 30; DB 1; Length 1451;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1430 CHSIC 1434

RESULT 87
US-08-331-625A-2
; Sequence 2, Application US/08331625A
; Patent No. 6057436
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,625A
; FILING DATE:
; CLASSIFICATION: 435
;
US-08-308-872B-4
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/880,194
;; FILING DATE: 08-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/698,927
;; FILING DATE: 13-MAY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/613,066
;; FILING DATE: 14-NOV-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Schreck, Patricia A.
;; REGISTRATION NUMBER: 33,777
;; REFERENCE/DOCKET NUMBER: SBC H85010-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 270-5015
;; TELEFAX: (215) 270-5090
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1452 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-331-625A-2

Query Match 88.2%; Score 30; DB 3; Length 1452;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1431 CHSIC 1435

RESULT 88
US-09-494-151-2
; Sequence 2, Application US/09494151
; Patent No. 6372224
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Klepfer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 270-5015
;; TELEFAX: (215) 270-5090
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1452 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-494-151-2

Query Match 88.2%; Score 30; DB 3; Length 1452;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1431 CHSIC 1435

RESULT 89
US-09-972-484-2
; Sequence 2, Application US/09972484
; Patent No. 6602504
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; Klepfer, Sharon
; Reed, Albert Paul
; Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; Therefor
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,484
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/494,151
; FILING DATE: 28-Jan-2000
; APPLICATION NUMBER: 08/331,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 270-5015
;; TELEFAX: (215) 270-5090
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1452 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-972-484-2

Query Match 88.2%; Score 30; DB 4; Length 1452;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1431 CHSIC 1435

RESULT 90

PCT-US93-04384-18
; Sequence 18, Application PC/TUS9304384
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Compositions and Methods for Vaccination
; TITLE OF INVENTION: Against Coronaviruses
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04384
; FILING DATE: 19930507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,171
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85009-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-04384-18

Query Match 88.2%; Score 30; DB 5; Length 1452;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1431 CHSIC 1435

RESULT 91

PCT-US93-04692-2

; Sequence 2, Application PC/TUS9304692
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Canine Coronavirus S Gene and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04692
; FILING DATE: 19930507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/880,194
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85010-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-04692-2

Query Match 88.2%; Score 30; DB 5; Length 1452;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1431 CHSIC 1435

RESULT 92

US-08-392-459-22
; Sequence 22, Application US/08392459
; Patent No. 6280974
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia

```
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,459
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-392-459-22

Query Match 88.2%; Score 30; DB 3; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1433 CHSIC 1437

RESULT 93
; US-08-392-459-26
; Sequence 26, Application US/08392459
; Patent No. 6280974
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,459
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-392-459-26

Query Match 88.2%; Score 30; DB 3; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1433 CHSIC 1437

RESULT 94
; US-09-854-799-22
; Sequence 22, Application US/09854799
; Patent No. 6642359
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,799
; FILING DATE: 14-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,459
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-09-854-799-22

Query Match 88.2%; Score 30; DB 4; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 95
US-09-854-799-26
; Sequence 26, Application US/09854799
; Patent No. 6642359
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
;   Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,799
; FILING DATE: 14-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,459
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1454 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-854-799-26
Query Match      88.2%; Score 30; DB 4; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 96
PCT-US91-08525-22
; Sequence 22, Application PC/TUS9108525
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
;   Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia

```

```

; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08525
; FILING DATE: 19911114
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1454 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-08525-22

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 97
PCT-US91-08525-26
; Sequence 26, Application PC/TUS9108525
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; TITLE OF INVENTION: Recombinant Feline Coronavirus S
;   Proteins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08525
; FILING DATE: 19911114
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:

```



```
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: SBC 14532B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-08525-26

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 98
PCT-US93-04384-2
; Sequence 2, Application PC/TUS9304384
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Compositions and Methods for Vaccination
; TITLE OF INVENTION: Against Coronaviruses
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04384
; FILING DATE: 19930507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,171
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85009-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-08525-26

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 99
PCT-US93-04384-8
; Sequence 8, Application PC/TUS9304384
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Compositions and Methods for Vaccination
; TITLE OF INVENTION: Against Coronaviruses
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04384
; FILING DATE: 19930507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,171
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85009-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-04384-8

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 100
```

```
PCT-US93-04384-2

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 99
PCT-US93-04384-8
; Sequence 8, Application PC/TUS9304384
; GENERAL INFORMATION:
; APPLICANT: Miller, Timothy J.
; APPLICANT: Klepfer, Sharon
; APPLICANT: Reed, Albert Paul
; APPLICANT: Jones, Elaine V.
; TITLE OF INVENTION: Compositions and Methods for Vaccination
; TITLE OF INVENTION: Against Coronaviruses
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04384
; FILING DATE: 19930507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/882,171
; FILING DATE: 08-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/698,927
; FILING DATE: 13-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/613,066
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: SBC H85009-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5015
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1454 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-04384-8

Query Match      88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      1433 CHSIC 1437

RESULT 100
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PCT-US93-04384-16
: Sequence 16, Application PC/TUS9304384
: GENERAL INFORMATION:
: APPLICANT: Miller, Timothy J.
: APPLICANT: Klepfer, Sharon
: APPLICANT: Reed, Albert Paul
: APPLICANT: Jones, Elaine V.
: TITLE OF INVENTION: Compositions and Methods for Vaccination
: TITLE OF INVENTION: Against Coronaviruses
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation - Corporate
: ADDRESSEE: Patents
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-2799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/04384
: FILING DATE: 19930507
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/882,171
: FILING DATE: 08-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/698,927
: FILING DATE: 13-MAY-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/613,066
: FILING DATE: 14-NOV-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Schreck, Patricia A.
: REGISTRATION NUMBER: 33,777
: REFERENCE/DOCKET NUMBER: SBC H85009-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 270-5015
: TELEFAX: (215) 270-5090
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1454 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US93-04384-16

Query Match 88.2%; Score 30; DB 5; Length 1454;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1433 CHSIC 1437

Search completed: July 27, 2005, 00:02:32
Job time : 42 secs

ALIGNMENTS

RESULT 1

E84885
hypothetical protein At2g45010 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84885
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-244 <STO>
A:Cross-references: UNIPROT:Q8L3TO; GB:AE002093; NID:g4895249; PIDN:AAD32834.1; GSPDB:GN
C:Genetics:
A:Gene: At2g45010
A:Map position: 2

Query Match 100.0%; Score 34; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 106 CHAVC 110

RESULT 2

MNXRPC
nonstructural protein NS34 - porcine rotavirus C (strain Cowden)
C:Species: porcine rotavirus C
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A41040
R:Qian, Y.; Jiang, B.; Saif, L.J.; Kang, S.Y.; Ojeh, C.K.; Green, K.Y.
Virology 184, 752-757, 1991
A:Title: Molecular analysis of the gene 6 from a porcine group C rotavirus that encodes
A:Reference number: A41040; MUID:91361567; PMID:1653496
A:Accession: A41040
A:Molecule type: genomic RNA
A:Residues: 1-402 <QIA>
A:Cross-references: UNIPROT:P27586; GB:M69115; NID:g333307; PIDN:AAA47087.1; PID:g333308
C:Genetics:
A:Map position: segment 6
C:Superfamily: rotavirus nonstructural protein
C:Keywords: nonstructural protein

Query Match 97.1%; Score 33; DB 1; Length 402;
Best Local Similarity 80.0%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 280 CHAIC 284

RESULT 3

S35639
hypothetical protein - bovine rotavirus C
C:Species: bovine rotavirus C
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S35639
R:Jiang, B.; Tsunemitsu, H.; Gentsch, J.R.; Saif, L.J.; Glass, R.I.
Nucleic Acids Res. 21, 2250, 1993
A:Title: Nucleotide sequences of genes 6 and 10 of a bovine group C rotavirus.
A:Reference number: S35639; MUID:93275758; PMID:8389040
A:Accession: S35639
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-402 <JIA>
A:Cross-references: UNIPROT:P34717; EMBL:L12390
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1993
C:Superfamily: rotavirus nonstructural protein

Query Match 97.1%; Score 33; DB 2; Length 402;
Best Local Similarity 80.0%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 280 CHAIC 284

RESULT 4

T48008
hypothetical protein T17J13.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48008
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, I.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24482
A:Accession: T48008
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <RIE>
A:Cross-references: UNIPROT:Q9MIQ8; EMBL:AL138651
A:Experimental source: cultivar Columbia; BAC clone T17J13
C:Genetics:
A:Map position: 3
A:Introns: 137/3
A:Note: T17J13.120

Query Match 97.1%; Score 33; DB 2; Length 428;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 153 CHAIC 157

RESULT 5

A4276
noncapsid protein NS1 - parvovirus LuIII
C:Species: parvovirus LuIII
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: A44276
R:Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, M.
Virology 192, 339-345, 1993
A:Title: The complete nucleotide sequence of parvovirus LuIII and localization of a unique
A:Reference number: A44276; MUID:93297126; PMID:8517025
A:Accession: A44276
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-668 <DIF>
A:Cross-references: UNIPROT:P36311; GB:M81888
C:Superfamily: parvovirus noncapsid protein
C:Keywords: noncapsid protein

Query Match 97.1%; Score 33; DB 1; Length 668;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:
Db 378 CHAIC 382

RESULT 6

UYPVIM

noncapsid protein NS1 - minute virus of mice
 C:Species: minute virus of mice, murine parvovirus
 C>Date: 14-Nov-1983 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
 C:Accession: A03696
 R:Atccll, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C.
 Nucleic Acids Res. 11, 999-1018, 1983
 A:Title: The complete DNA sequence of minute virus of mice, an autonomous parvovirus.
 A:Reference number: A03696; MUID:83143341; PMID:6298737
 A:Accession: A03696
 A:Molecule type: DNA
 A:Residues: 1-672 <AST>
 A:Cross-references: UNIPROT:P03134; EMBL:V01115
 C:Superfamily: parvovirus noncapsid protein
 C:Keywords: noncapsid protein

Query Match 97.1%; Score 33; DB 1; Length 672;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 378 CHAIC 382

RESULT 7
 UVPV1
 noncapsid protein NS1 - parvovirus H1
 C:Species: parvovirus H1
 A:Note: host Homo sapiens (man)
 C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
 C:Accession: A03695
 R:Rhode III, S.L.; Paradiso, P.R.
 J. Virol. 45, 173-184, 1983
 A:Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybridization
 A:Reference number: A03695; MUID:83112183; PMID:6823009
 A:Accession: A03695
 A:Molecule type: DNA
 A:Residues: 1-672 <RHO>
 A:Cross-references: UNIPROT:P03133; EMBL:X01457; NID:g60993; PIDN:CAA25689.1; PID:g60994
 C:Superfamily: parvovirus noncapsid protein
 C:Keywords: noncapsid protein

Query Match 97.1%; Score 33; DB 1; Length 672;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 378 CHAIC 382

RESULT 8
 UVPV1M
 noncapsid protein NS1 - minute virus of mice (strain MVMi)
 C:Species: minute virus of mice, murine parvovirus
 C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C:Accession: A23008; A29510
 R:Sanli, R.; McMaster, G.K.; Hirt, B.
 Nucleic Acids Res. 13, 3617-3633, 1985
 A:Title: DNA sequence comparison between two tissue-specific variants of the autonomous parvovirus genome
 A:Reference number: A23008; MUID:85242059; PMID:3855242
 A:Accession: A23008
 A:Molecule type: DNA
 A:Residues: 1-721 <SAH>
 A:Cross-references: UNIPROT:Q84363; EMBL:X02481
 R:Atccll, C.R.; Gardiner, E.M.; Tattersall, P.
 J. Virol. 57, 656-669, 1986
 A:Title: DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and of the nonautonomous variant MVM(i)ns
 A:Reference number: A29510; MUID:86115415; PMID:3502703
 A:Accession: A29510
 A:Molecule type: DNA
 A:Residues: 1-645, 'I', 647-721 <AST>
 A:Cross-references: EMBL:M12032; NID:g332289; PIDN:AAA69566.1; PID:g825477

C:Superfamily: parvovirus noncapsid protein
 C:Keywords: noncapsid protein

Query Match 97.1%; Score 33; DB 1; Length 721;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 427 CHAIC 431

RESULT 9
 S09903
 hypothetical protein IRL10 precursor - human cytomegalovirus (strain AD169)
 C:Species: human cytomegalovirus, human herpesvirus 5
 A:Note: host Homo sapiens (man)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: S09903
 R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohnl, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; M.; Barrell, B.G.
 Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
 A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
 A:Reference number: S09749; MUID:90269039; PMID:2161319
 A:Accession: S09903
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-171 <CHE>
 A:Cross-references: UNIPROT:P16808; EMBL:X17403; NID:g59591; PIDN:CAA35300.1; PID:g17809
 A:Note: this sequence was submitted to the EMBL Data Library, December 1989
 C:Keywords: glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-171/Product: hypothetical protein IRL10 #status predicted <MAT>
 F:70-103/Domain: transmembrane #status predicted <TM>
 F:48,49,56,108/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.2%; Score 31; DB 2; Length 171;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 60 CHAMC 64

RESULT 10
 S09759
 hypothetical protein TRIL0 precursor - human cytomegalovirus (strain AD169)
 C:Species: human cytomegalovirus, human herpesvirus 5
 A:Note: host Homo sapiens (man)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: S09759
 R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohnl, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; M.; Barrell, B.G.
 Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
 A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
 A:Reference number: S09749; MUID:90269039; PMID:2161319
 A:Accession: S09759
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-171 <CHE>
 A:Cross-references: UNIPROT:Q69029; EMBL:X17403; NID:g59591; PIDN:CAA35458.1; PID:g59601
 A:Note: this sequence was submitted to the EMBL Data Library, December 1989
 C:Keywords: glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-171/Product: hypothetical protein TRIL0 #status predicted <MAT>
 F:70-103/Domain: transmembrane #status predicted <TM>
 F:48,49,56,108/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.2%; Score 31; DB 2; Length 171;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 60 CHAVC 64

RESULT 11

S34794
osmotin - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S34794; S37294
R:Singh, N.K.; Nelson, D.E.; Kuhn, D.; Hasegawa, P.M.; Bressan, R.A.
Plant Physiol. 90, 1096-1101, 1989
A:Title: Molecular cloning of osmotin and regulation of its expression by ABA and adaptation
A:Reference number: S34794
A:Accession: S34794
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-243 <SIN>
A:Cross-references: UNIPROT:P14170; EMBL:M29279
R:Singh, N.K.; Nelson, D.E.; Kuhn, D.; Hasegawa, P.M.; Bressan, R.A.
submitted to the EMBL data library, February 1990
A:Reference number: S37294
A:Accession: S37294
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128, 17, 130-243 <ST2>
A:Cross-references: EMBL:M29279; NID:gl70278; PIDN:AAA34089.1; PID:gl70279
C:Superfamily: thaumatin I

Query Match 91.2%; Score 31; DB 2; Length 243;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 140 CHALC 144

RESULT 12

E86378
protein F21J9.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86378
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86378
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <STO>
A:Cross-references: UNIPROT:Q9FYL9; GB:AE005172; NID:g9743332; PIDN:AAF97956.1; GSPDB:GN
C:Genetics:

A:Gene: F21J9.10
A:Map position: 1
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.40; RING finger homology

Query Match 91.2%; Score 31; DB 2; Length 251;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 171 CHAVC 175

RESULT 13

YXMS1
thymidylate synthase (EC 2.1.1.45) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Aug-2004
C:Accession: A26323; A24157; I48858
R:Deng, T.; Li, D.; Jenh, C.H.; Johnson, L.F.
J. Biol. Chem. 261, 16000-16005, 1986
A:Title: Structure of the gene for mouse thymidylate synthase. Locations of introns and n
plant Physiol. 90, 1096-1101, 1989
A:Reference number: A26323; MUID:87057259; PMID:3782103
A:Accession: A26323

A:Molecule type: DNA
A:Residues: 1-307 <DEN>
A:Cross-references: UNIPROT:P07607; GB:M13352; NID:g202048; PIDN:AAA40444.1; PID:g202050
R:Perryman, S.M.; Rossana, C.; Deng, T.; Vanin, E.F.; Johnson, L.F.
Mol. Biol. Evol. 3, 313-321, 1986
A:Title: Sequence of a cDNA for mouse thymidylate synthase reveals striking similarity w
A:Reference number: A24157; MUID:88174353; PMID:3444407
A:Accession: A24157
A:Molecule type: mRNA
A:Residues: 1-307 <PER>
A:Cross-references: GB:M13019; NID:g202029; PIDN:AAA40439.1; PID:g202030
R:Deng, T.L.; Li, Y.; Johnson, L.F.
Nucleic Acids Res. 17, 645-658, 1989
A:Title: Thymidylate synthase gene expression is stimulated by some (but not all) introns
A:Reference number: I48858; MUID:89128436; PMID:2915925
A:Accession: I48858
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 236-265 <RES>
A:Cross-references: EMBL:X14489; NID:g54931; PIDN:CAA32651.1; PID:g899339
C:Genetics:
A:Introns: 63/1; 87/3; 146/1; 180/1; 238/3; 262/3
C:Superfamily: Thymidylate synthase; thymidylate synthase homology
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F:24-307/Domain: thymidylate synthase homology <TDS>
F:193/Active site: Cys #status predicted

Query Match 91.2%; Score 31; DB 1; Length 307;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 189 CHALC 193

RESULT 14

S53715
thymidylate synthase (EC 2.1.1.45) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S53715
R:Ciesla, J.; Weiner, K.X.B.; Weiner, R.S.; Reston, J.T.; Maley, G.F.; Maley, F.
Biochim. Biophys. Acta 1261, 233-242, 1995
A:Title: Isolation and expression of rat thymidylate synthase cDNA: phylogenetic compari
A:Reference number: S53715; MUID:95226450; PMID:7711067
A:Accession: S53715
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-307 <CIE>
A:Cross-references: UNIPROT:P45352; EMBL:L12138; NID:g207327; PIDN:AAA92340.1; PID:g20732
C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: methyltransferase
F:24-307/Domain: thymidylate synthase homology <TDS>

Query Match 91.2%; Score 31; DB 2; Length 307;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 189 CHALC 193

RESULT 15

YXHU7

thymidylate synthase (EC 2.1.1.45) - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Aug-2004
C/Accession: A23047; J00120; A22393; A33842
R/Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.
Nucleic Acids Res. 13, 2035-2043, 1985
A/Title: Nucleotide sequence of a functional cDNA for human thymidylate synthase.
A/Reference number: A23047; MUID:85215597; PMID:2987839
A/Accession: A23047
A/Molecule type: mRNA
A/Residues: 1-313 <TAK>
A/Cross-references: UNIPROT:P04818; EMBL:X02308; NID:g37478; PIDN:CAA26178.1; PID:g37479
R/Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.; Ayusawa, J. Biol. Chem. 265, 20277-20284, 1990
A/Title: Structural and Functional Analysis of the Human Thymidylate Synthase Gene.
A/Reference number: 155318; MUID:91056070; PMID:2243092
A/Accession: 155318
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-313 <RES>
A/Cross-references: GB:D00596; NID:g220135; PIDN:BAA00472.1; PID:g220136
R/Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.
J. Biochem. 106, 575-583, 1989
A/Title: Human thymidylate synthase gene: isolation of phage clones which cover a functional cDNA.
A/Reference number: J00120; MUID:90110051; PMID:2532645
A/Accession: J00120
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-68 <TA2>
A/Cross-references: GB:D00517; NID:g220133; PIDN:BAA00404.1; PID:g2160415
R/Shimizu, K.; Ayusawa, D.; Takeishi, K.; Seno, T.
J. Biochem. 97, 845-850, 1995
A/Title: Purification and NH2-terminal amino acid sequence of human thymidylate synthase
A/Reference number: A22393; MUID:85261174; PMID:3839505
A/Accession: A22393
A/Molecule type: protein
A/Residues: 2-25 <SHI>
R/Davisson, V.J.; Sirawaraporn, W.; Santi, D.V.
J. Biol. Chem. 264, 9145-9148, 1989
A/Title: Expression of human thymidylate synthase in Escherichia coli.
A/Reference number: A33842; MUID:89255401; PMID:2655695
A/Accession: A33842
A/Molecule type: protein
A/Residues: 2-10 <DAV>
C/Genetics:
A/Gene: GDB:TYMS
A/Cross-references: GDB:120465; OMIM:188350
A/Map position: 18p11.32-18p11.32
A/Introns: 69/1; 93/3; 152/1; 186/1; 244/3; 268/3
C/Superfamily: Thymidylate synthase; thymidylate synthase homology
C/Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F/30-313/Domain: thymidylate synthase homology <TDS>
F/190/Active site: Cys #status predicted

Query Match 91.2%; Score 31; DB 1; Length 313;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 195 CHALC 199

RESULT 16

T25920

hypothetical protein T27A3.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T25920
R/Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, February 1997
A/Description: The sequence of C. elegans cosmid T27A3.
A/Reference number: 220110

A/Accession: T25920
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-373 <MUR>
A/Cross-references: UNIPROT:P91501; EMBL:U88180; PIDN:AAB42300.1; GSPDB:GN00019; CESP:T2
A/Experimental source: strain Bristol N2; Clone T27A3
C/Genetics:
A/Gene: CESP:T27A3.7
A/Map position: 1
A/Introns: 80/1; 113/3; 154/2; 211/3; 273/2
C/Superfamily: Caenorhabditis elegans hypothetical protein T27A3.7

Query Match 91.2%; Score 31; DB 2; Length 373;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 262 CHALC 266

RESULT 17

A69335
succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C/Accession: A69335
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A/Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A/Reference number: A69250; MUID:98049343; PMID:9389475
A/Accession: A69335
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-563 <KLE>
A/Cross-references: UNIPROT:O29576; GB:AE001057; GB:AE000782; NID:g2689380; PIDN:AAB9055
C/Superfamily: Succinate dehydrogenase flavoprotein subunit; 3-oxosteroid 1-dehydrogenase
C/Keywords: FAD; flavoprotein; oxidoreductase
F/4-265/Domain: fumarate reductase flavoprotein homology <PRF>
F/297-389/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>

Query Match 91.2%; Score 31; DB 2; Length 563;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 41 CHSVC 45

RESULT 18

G87753
protein C43E11.8 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G87753
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:95069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: G87753

F;25-645/Domain: extracellular #status predicted <EXT>
 F;75-300/Domain: EGF receptor extracellular domain repeat <EE1>
 F;390-600/Domain: EGF receptor extracellular domain repeat <EE2>
 F;646-668/Domain: transmembrane #status predicted <TM>
 F;669-1210/Domain: intracellular #status predicted <INT>
 F;710-975/Domain: protein kinase homology <KIN>
 F;718-726/Region: protein kinase ATP-binding motif
 F;999-1046/Region: coated-pit mediated internalization signal
 F;1047-1210/Region: inhibitory
 F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn)
 F;745/Active site: Lys #status experimental

Query Match 91.2%; Score 31; DB 1; Length 1210;
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 506 CHALC 510

RESULT 21

T34264

hypothetical protein F46C8.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T34264

R;Wilcox, L.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid F46C8.

A;Reference number: Z21497

A;Accession: T34264

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2195 <WIL>

A;Cross-references: EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4

C;Genetics:

A;Gene: CESP:F46C8.4

A;Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/1; 466/1; 507/2; 629/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1

Query Match 91.2%; Score 31; DB 2; Length 2195;
 Best Local Similarity 80.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 136 CHSVC 140

RESULT 22

E96980

hypothetical protein CAC0655 [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: E96980

R;Nolling, J.; Brston, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: E96980

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <KUR>

A;Cross-references: UNIPROT:Q971A7; GB:AE001437; PIDN:AAK78632.1; PID:gl5023530; GSPDB:G

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC0655

Query Match 88.2%; Score 30; DB 2; Length 67;
 Best Local Similarity 80.0%; Pred. No. 84;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 21 CHCVC 25

RESULT 23

T25293

hypothetical protein T26E3.7 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T25293

R;Kershaw, J.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20012

A;Accession: T25293

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-106 <WIL>

A;Cross-references: UNIPROT:O45827; EMBL:Z82053; PIDN:CAB04832.1; GSPDB:GN00019; CESP:T2

A;Experimental source: clone T26E3

C;Genetics:

A;Gene: CESP:T26E3.7

A;Map position: 1

A;Introns: 81/2

Query Match 88.2%; Score 30; DB 2; Length 106;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 53 CHVVC 57

RESULT 24

AG2472

hypothetical protein alx535 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG2472

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <KUR>

A;Cross-references: UNIPROT:Q8YLG3; GB:BA000019; PIDN:BAW77034.1; PID:gl7134474; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alx535

Query Match 88.2%; Score 30; DB 2; Length 108;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
 Db 11 CHSIC 15

RESULT 25

AG2543

hypothetical protein alx7634 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120b6

C;Species: *Nostoc* sp. PCC 7120

A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AG2543

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Rep. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AG2543
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-122 <KUR>
 A:Cross-references: UNIPROT:Q8ZS78; GB:AP003602; PIDN:BA877277.1; PID:gl17134719; GSPDB:C
 A:Experimental source: strain FCC 7120
 C:Genetics:
 A:Gene: alr7634
 A:Genome: plasmid

Query Match
 Best Local Similarity 88.2%; Score 30; DB 2; Length 122;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 ||:|
 Db 25 CHSIC 29

RESULT 26
 A86086
 hypothetical protein yijI [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: A86086
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A86086
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <STO>
 A:Cross-references: UNIPROT:Q8X758; GB:AE005174; NID:gl2518866; PIDN:AAG59149.1; GSPDB:C
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: yijI

Query Match
 Best Local Similarity 88.2%; Score 30; DB 2; Length 154;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 ||:|
 Db 86 CHSIC 90

RESULT 27
 E91238
 hypothetical protein ECs4876 [imported] - Escherichia coli (strain O157:H7, substrain RIMD
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: E91238
 R:Hayashi, T.; Makino, K.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Rep. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: E91238
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-163 <HAY>
 A:Cross-references: UNIPROT:Q8X758; GB:BA000007; PIDN:BA838300.1; PID:gl13364353; GSPDB:C
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs4876

Query Match
 Best Local Similarity 88.2%; Score 30; DB 2; Length 163;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 60.0%; Pred. No. 1.6e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 ||:|
 Db 95 CHSIC 99

RESULT 28
 T25841
 hypothetical protein M03F4.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T25841
 R:Fulton, L.
 submitted to the EMBL Data Library, July 1996
 A:Description: The sequence of C. elegans cosmid M03F4.
 A:Reference number: Z20097
 A:Accession: T25841
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-179 <FUL>
 A:Cross-references: EMBL:U64601; PIDN:AAB04577.1; GSPDB:GN000028; CESP:M03F4.6
 A:Experimental source: strain Bristol N2; clone M03F4
 C:Genetics:
 A:Gene: CESP:M03F4.6
 A:Map position: X
 A:Introns: 41/1; 129/2

Query Match
 Best Local Similarity 88.2%; Score 30; DB 2; Length 179;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
 ||:|
 Db 38 CHATC 42

RESULT 29
 IVHOAI
 interferon alpha-I-1 precursor - horse
 N:Alternate names: EqIFN-alpha-I-1; type I interferon
 C:Species: Equus caballus (domestic horse)
 C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C:Accession: A24912
 R:Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
 DNA 5, 345-356, 1986
 A:Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
 A:Reference number: A30956; MUID:87053170; PMID:3022999
 A:Accession: A24912
 A:Molecule type: DNA
 A:Residues: 1-184 <HIM>
 A:Cross-references: UNIPROT:P05003; GB:M14540; NID:gl64226; PIDN:AAA30953.1; PID:gl64227
 C:Superfamily: interferon alpha
 C:Keywords: antiviral
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-184/Product: interferon alpha-I-1 #status predicted <MAT>
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match
 Best Local Similarity 88.2%; Score 30; DB 1; Length 184;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 ||:|
 Db 16 CHSIC 20

RESULT 30
 T34728
 hypothetical protein SC186.07 SC186.07 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T34728
 R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, November 1998
 A;Reference number: Z21555
 A;Accession: T34728
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-319 <SEE>
 A;Cross-references: UNIPROT:Q92C15; EMBL:AL033505; PIDN:CAA22035.1; GSPDB:GN00070; SCORE1
 A;Experimental source: strain A3(2)
 C;Genetics:
 C;Superfamily: Streptomyces coelicolor hypothetical protein SC4C6.19
 A;Gene: SC0DB:SC1E6.07
 Query Match 88.2%; Score 30; DB 2; Length 319;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 111 CHTVC 115
 RESULT 31
 F70467
 hypothetical protein aq_1958 - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C;Accession: F70467
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
 V.
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: F70467
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-372 <AOP>
 A;Cross-references: UNIPROT:O67770; GB:AE000765; NID:g2984199; PIDN:AAAC07741.1; PID:g298
 A;Experimental source: strain VP5
 C;Genetics:
 A;Gene: aq_1958
 Query Match 88.2%; Score 30; DB 2; Length 372;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 55 CHATC 59
 RESULT 32
 DEMSAA
 alcohol dehydrogenase (EC 1.1.1.1) A - mouse
 N;Alternate names: alcohol dehydrogenase beta
 C;Species: Mus musculus (house mouse)
 C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 09-Jul-2004
 C;Accession: A27322; A29628; A00338; S50103; A25849
 R;Zhang, K.; Bosron, W.F.; Edenberg, H.J.
 Gene 57, 27-36, 1987
 A;Title: Structure of the mouse Adh-1 gene and identification of a deletion in a long al
 ty.
 A;Reference number: A27322; MUID:88112859; PMID:3428612
 A;Accession: A27322
 A;Molecule type: DNA
 A;Residues: 1-375 <ZHA>
 A;Cross-references: UNIPROT:P00329; GB:M11307; NID:g191717; PIDN:AAA37180.1; PID:g309094
 R;Ceci, J.D.; Zheng, Y.W.; Felder, M.R.
 Gene 59, 171-182, 1987
 A;Title: Molecular analysis of mouse alcohol dehydrogenase: nucleotide sequence of the A
 A;Reference number: A29628; MUID:88137953; PMID:2893758
 A;Accession: A29628

A;Molecule type: DNA
 A;Residues: 1-375 <CEC>
 A;Cross-references: GB:M22611
 R;Edenberg, H.J.; Zhang, K.; Fong, K.; Bosron, W.F.; Li, T.K.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2262-2266, 1985
 A;Title: Cloning and sequencing of cDNA encoding the complete mouse liver alcohol dehydr
 A;Reference number: A00338; MUID:85190477; PMID:3157987
 A;Accession: A00338
 A;Molecule type: mRNA
 A;Residues: 1-375 <EDE>
 A;Cross-references: GB:M11307; NID:g191717; PIDN:AAA37180.1; PID:g309094
 A;Note: in Genbank entry MUSADH1A, release 109.0, the source is designated as Mus caroli
 R;Caubin, J.; Iglesias, T.; Bernal, J.; Munoz, J.; Marquez, G.; Barbero, J.L.; Zaball
 Nucleic Acids Res. 22, 4132-4138, 1994
 A;Title: Isolation of genomic DNA fragments corresponding to genes modulated in vivo by
 A;Reference number: S50102; MUID:95023181; PMID:7937138
 A;Accession: S50103
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 8-51 <CAU>
 A;Cross-references: EMBL:Z32540
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
 R;Ceci, J.D.; Lawther, R.; Duester, G.; Hatfield, G.W.; Smith, M.; O'Malley, M.P.; Felde
 Gene 41, 217-224, 1986
 A;Title: Androgen induction of alcohol dehydrogenase in mouse kidney. Studies with a cDN
 A;Reference number: A25849; MUID:86221702; PMID:3011597
 A;Accession: A25849
 A;Molecule type: mRNA
 A;Residues: 224-375 <CE2>
 A;Cross-references: GB:M22611; NID:g191719; PIDN:AAA37181.1; PID:g191720
 C;Comment: This enzyme converts primary and secondary alcohols to aldehydes using NAD as
 C;Comment: The active enzyme is a dimer of identical or nonidentical zinc-containing pol
 C;Genetics:
 A;Gene: Adh-1
 A;Introns: 6/3; 40/3; 87/1; 116/2; 189/3; 276/3; 322/1; 368/2
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor
 F;2-375/Product: alcohol dehydrogenase chain A #status predicted <MAI>
 F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
 F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted
 Query Match 88.2%; Score 30; DB 1; Length 375;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 283 CHAAC 287
 RESULT 33
 A39556
 triacylglycerol lipase (EC 3.1.1.3) 2 - Moraxella sp. (strain TA144)
 C;Species: Moraxella sp.
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: A39556
 R;Feller, G.; Thiry, M.; Gerdard, C.
 DNA Cell Biol. 10, 381-388, 1991
 A;Title: Nucleotide sequence of the lipase gene lip2 from the antarctic psychrotroph Mor
 A;Reference number: A39556; MUID:91321741; PMID:1907455
 A;Accession: A39556
 A;Molecule type: DNA
 A;Residues: 1-433 <FEL>
 A;Cross-references: UNIPROT:P24484; GB:X53868; NID:g296841; PIDN:CAA37862.1; PID:g296842
 C;Genetics:
 A;Gene: lip2
 C;Keywords: carboxylic ester hydrolase
 Query Match 88.2%; Score 30; DB 2; Length 433;
 Best Local Similarity 80.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
Db 181 CHTVC 185

RESULT 34
S64826
Probable membrane protein YLR004c - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein Ll515
C:Species: *Saccharomyces cerevisiae*
C>Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: S64826
R:Vandenbol, M.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64742
A:Accession: S64826
A:Molecule type: DNA
A:Residues: 1-523 <VAN>
A:Cross-references: UNIPROT:Q07904; EMBL:Z73176; NID:gl360291; PID:e245487; PID:gl360292
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YLR004C
A:Cross-references: SGD:S0003994
A:Map position: 12R
C:Keywords: transmembrane protein
F:78-94/Domain: transmembrane #status predicted <TM1>
F:123-139/Domain: transmembrane #status predicted <TM2>
F:147-163/Domain: transmembrane #status predicted <TM3>
F:242-258/Domain: transmembrane #status predicted <TM4>
F:345-361/Domain: transmembrane #status predicted <TM5>
F:379-395/Domain: transmembrane #status predicted <TM6>
F:467-483/Domain: transmembrane #status predicted <TM7>

Query Match 88.2%; Score 30; DB 2; Length 523;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
Db 161 CHAAC 165

RESULT 35
F86281
protein F10B6.14 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86281
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-760 <STO>
A:Cross-references: UNIPROT:Q9LQV7; GB:AE005172; NID:g8778236; PIDN:AAF79245.1; GSPDB:GN
C:Genetics:
A:Gene: F10B6.14
A:Map position: 1

Query Match 88.2%; Score 30; DB 2; Length 760;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
Db 464 CHAAC 468

RESULT 36

S5554
male-specific lethal 2 protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S5554
R:Zhou, S.; Yang, Y.; Scott, M.J.; Pannuti, A.; Fehr, K.C.; Eisen, A.; Koonin, E.V.; Fout,
EMBO J. 14, 2894-2895, 1995
A:Title: Male-specific lethal 2, a dosage compensation gene of *Drosophila*, undergoes sex
A:Reference number: S5554; MUID:95317307; PMID:7796814
A:Accession: S5554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-769 <ZHO>
A:Cross-references: UNIPROT:P50534; EMBL:Z48443; NID:g872110; PIDN:CAA88358.1; PID:g87211
C:Genetics:
A:Gene: FlyBase:msl-2
A:Cross-references: FlyBase:FBgn0005616
A:Introns: 641/1

Query Match 88.2%; Score 30; DB 2; Length 769;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
Db 552 CHVC 556

RESULT 37

A27131
epidermal growth factor receptor - fruit fly (*Drosophila melanogaster*) (fragment)
C:Species: *Drosophila melanogaster*
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A27131
R:Schejter, E.D.; Segal, D.; Glazer, L.; Shilo, B.2.
Cell 46, 1091-1101, 1986
A:Title: Alternative 5' exons and tissue-specific expression of the *Drosophila* EGF receptor
A:Reference number: A27131; MUID:87002474; PMID:3093080
A:Accession: A27131
A:Molecule type: mRNA
A:Residues: 1-843 <SCH>
A:Cross-references: UNIPROT:Q8MLW0
C:Genetics:
A:Gene: FlyBase:Egfr
A:Cross-references: FlyBase:FBgn0003731
A:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; growth factor receptor

Query Match 88.2%; Score 30; DB 2; Length 843;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
Db 619 CHATC 623

RESULT 38

B81704
conserved hypothetical protein TC024 [imported] - *Chlamydia muridarum* (strain Nigg)
C:Species: *Chlamydia muridarum*, *Chlamydia trachomatis* MoPn
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81704
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.P.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; deBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; UID:20150255; PMID:10684935
A;Accession: B81704
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1436 <TET>
A;Cross-references: UNIPROT:Q9PKP1; GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF3928
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0424

Query Match 88.2%; Score 30; DB 2; Length 1436;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1033 CHAAC 1037

RESULT 39
VG1HE3
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Purdue)
N;Alternate names: peplomer protein; spike glycoprotein
C;Species: porcine transmissible gastroenteritis virus
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 12-Apr-1996
C;Accession: J50336
R;Jacobs, L.; de Groot, R.; van der Zeijst, B.A.M.; Horzinek, M.C.; Spaan, W.
Virus Res. 8, 363-371, 1987
A;Title: The nucleotide sequence of the peplomer gene of porcine transmissible gastroenteritis virus (P1PV).
A;Reference number: J50336; UID:88129049; PMID:2829461
A;Accession: J50336
A;Molecule type: mRNA
A;Residues: 1-1447 <JAC>
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1447/Product: E2 glycoprotein #status predicted <WAT>
F;1397-1431/Domain: transmembrane #status predicted <TMM>
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91

Query Match 88.2%; Score 30; DB 1; Length 1447;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1426 CHSIC 1430

RESULT 40
VG1HE2
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Purdue-1)
N;Alternate names: spike glycoprotein
C;Species: porcine transmissible gastroenteritis virus
A;Variety: strain Purdue-115
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A27106; S01738
R;Raschaert, D.; Laude, H.
J. Gen. Virol. 68, 1883-1890, 1987
A;Title: The predicted primary structure of the peplomer protein E2 of the porcine coronavirus.
A;Reference number: A27106; UID:87253116; PMID:3037011
A;Accession: A27106
A;Molecule type: genomic RNA
A;Residues: 1-1447 <RAS>
A;Cross-references: UNIPROT:P07946; GB:X05695; GB:D00118; NID:g59007; PIDN:CAA29175.1; E
A;Experimental source: strain Purdue-115
R;Raschaert, D.; Gelfi, J.; Laude, H.
Biochimie 69, 591-600, 1987
A;Title: Enteric coronavirus TGEV: partial sequence of the genomic RNA, its organization
A;Reference number: S01738; UID:88078100; PMID:2825819
A;Accession: S01738

A;Molecule type: genomic RNA
A;Residues: 1434-1447 <RAW>
A;Cross-references: EMBL:X06371
A;Experimental source: strain Purdue-115
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1447/Product: E2 glycoprotein #status predicted <WAT>
F;1387-1431/Domain: transmembrane #status predicted <TMM>
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91
F;26,42,71,94,243,250,285,334,345,362,403,447,514,530,552,592,702,723,778,817,832,838,91

Query Match 88.2%; Score 30; DB 1; Length 1447;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1426 CHSIC 1430

RESULT 41
A43573
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain Miller)
N;Alternate names: peplomer glycoprotein; spike glycoprotein
C;Species: porcine transmissible gastroenteritis virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A43573
R;Weasley, R.D.
Adv. Exp. Med. Biol. 276, 301-306, 1990
A;Title: Nucleotide sequence of the E2-peplomer protein gene and partial nucleotide sequence of the E2-peplomer protein gene.
A;Reference number: A43573; UID:91353366; PMID:1966416
A;Accession: A43573
A;Molecule type: genomic RNA
A;Residues: 1-1449 <WES>
A;Cross-references: UNIPROT:P33470; GB:S51223; NID:g234109; PIDN:AAB19567.1; PID:g234110
A;Note: the authors translated the codon GAA for residue 388 as Cys
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>
F;1027-1043/Region: hydrophobic
F;1391-1411/Domain: transmembrane #status predicted <TMM>
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,84
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,84

Query Match 88.2%; Score 30; DB 1; Length 1449;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1428 CHSIC 1432

RESULT 42
VG1HFS
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain FS772/70)
N;Alternate names: peplomer glycoprotein; spike glycoprotein
C;Species: porcine transmissible gastroenteritis virus
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: B43489; S11728
R;Britton, P.; Page, K.W.
Virus Res. 18, 71-80, 1990
A;Title: Sequence of the S gene from a virulent British field isolate of transmissible gastroenteritis virus.
A;Reference number: A43489; UID:91188698; PMID:1964522
A;Accession: B43489
A;Molecule type: mRNA
A;Residues: 1-1449 <BRI>
A;Cross-references: UNIPROT:P18450; GB:X53128; NID:g61377; PIDN:CAA37285.1; PID:g61379
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>

F:1027-1043/Region: hydrophobic
F:1395-1411/Domain: transmembrane #status predicted <TM>
F:26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,844
d

Query Match 88.2%; Score 30; DB 1; Length 1449;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
||:|
Db 1428 CHSIC 1432

RESULT 43
S47423
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus
N:Alternate names: envelope protein; spike protein
C:Species: porcine transmissible gastroenteritis virus
C:Date: 23-Nov-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S65851; S47423
R:Chen, C.M.; Cavanagh, D.; Britton, P.
Virus Res. 38, 83-89, 1995
A:Title: Cloning and sequencing of a 8.4-kb region from the 3'-end of a Taiwanese viru
A:Reference number: S65850; MUID:96060227; PMID:8546012
A:Accession: S65851
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: genomic RNA
A:Residues: 1-1449 <CH2>
A:Cross-references: UNIPROT:Q88510; EMBL:Z35759; NID:G529246; PIDN:CAA84806.1; PID:G52924
A:Experimental source: Taiwanese field isolate
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C:Genetics:
A:Gene: S
C:Superfamily: coronavirus E2 glycoprotein
C:Keywords: glycoprotein; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1449/Product: E2 glycoprotein #status predicted <E2G>

Query Match 88.2%; Score 30; DB 2; Length 1449;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
||:|
Db 1428 CHSIC 1432

RESULT 44
JQ1719
E2 glycoprotein precursor - canine coronavirus (strain Insvacv-1)
N:Alternate names: spike glycoprotein
C:Species: canine coronavirus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: JQ1719
R:Horsburgh, B.C.; Brierley, I.; Brown, T.D.K.
J. Gen. Virol. 73, 2849-2862, 1992
A:Title: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNA
A:Reference number: PQ0481; MUID:93057357; PMID:1431811
A:Accession: JQ1719
A:Molecule type: genomic RNA
A:Residues: 1-1451 <HOR>
A:Cross-references: UNIPROT:P36300; DBJ:DJ13096; NID:G406193; PIDN:BAA02408.1; PID:G4061
C:Genetics:
A:Gene: S
C:Superfamily: coronavirus E2 glycoprotein
C:Keywords: glycoprotein; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1451/Product: spike glycoprotein #status predicted <MAT>
F:1394-1412/Domain: transmembrane #status predicted <TM>
F:28,66,94,142,175,209,235,242,289,338,349,366,379,409,453,520,536,557,707,728,783,821,8
d

Query Match 88.2%; Score 30; DB 1; Length 1451;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
||:|
Db 1430 CHSIC 1434

RESULT 45
VG1H79
E2 glycoprotein precursor - feline infectious peritonitis virus (strain 79-1146)
N:Alternate names: peplomer glycoprotein; spike glycoprotein
C:Species: feline infectious peritonitis virus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A27171
R:De Groot, R.J.; Maduro, J.; Lenstra, J.A.; Horzinek, M.C.; Van Der Zeijst, B.A.M.; Spa
J. Gen. Virol. 68, 2639-2646, 1987
A:Title: cDNA cloning and sequence analysis of the gene encoding the peplomer protein of
A:Reference number: A27171; MUID:88034948; PMID:3312491
A:Accession: A27171
A:Molecule type: genomic RNA
A:Residues: 1-1452 <DEG>
A:Cross-references: UNIPROT:P10033; GB:X06170; GB:D00150; NID:G58915; PIDN:CAA29535.1; PI
C:Superfamily: coronavirus E2 glycoprotein
C:Keywords: glycoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1452/Product: spike glycoprotein #status predicted <SPG>
F:1394-1414/Domain: transmembrane #status predicted <TM2>
F:29,95,174,208,234,241,288,337,348,365,408,452,483,519,535,557,565,707,728,783,822,837,8
ted

Query Match 88.2%; Score 30; DB 1; Length 1452;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
||:|
Db 1431 CHSIC 1435

RESULT 46
S41453
spike protein - canine coronavirus
C:Species: canine coronavirus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41453
R:Wesseling, J.G.; Vennema, H.; Godeke, G.J.; Spaan, W.J.M.; Horzinek, M.C.; Rottier, P.
submitted to the EMBL Data Library, December 1993
A:Description: Nucleotide sequence and expression of the spike (S) gene of canine coronav
A:Reference number: S41453
A:Accession: S41453
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1453 <WES>
A:Cross-references: UNIPROT:Q65984; EMBL:X77047; NID:G452379; PIDN:CAA54335.1; PID:G45237
C:Superfamily: coronavirus E2 glycoprotein

Query Match 88.2%; Score 30; DB 2; Length 1453;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
||:|
Db 1432 CHSIC 1436

RESULT 47
A42125
trophozoite cysteine-rich surface antigen 170 - Giardia lamblia
N:Alternate names: CRP170; cysteine-rich surface antigen CRP170
C:Species: Giardia lamblia

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C;Accession: A42125; B42125; S00530; S48056
 R;Adam, R.D.; Yang, Y.M.; Nash, T.E.
 Mol. Cell. Biol. 12, 1194-1201, 1992
 A;Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170 gene
 A;Reference number: A42125; MUID:92186850; PMID:1545800
 A;Accession: A42125
 A;Molecule type: DNA
 A;Residues: 1-98 <ADA1>
 A;Cross-references: UNIPROT:P15799; GB:M83937; NID:g159124
 A;Experimental source: trophozoite
 A;Note: sequence extracted from NCBI backbone (NCBIN:88421, NCBI:P:88427); this ORF is not
 A;Note: the authors report but do not show 19 tandem repeats of the sequence of residues
 A;Accession: B42125
 A;Molecule type: DNA
 A;Residues: 1269-1766 <ADA2>
 A;Cross-references: GB:M83933; NID:g159122
 A;Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBI:P:88431); this ORF is not
 R;Adam, R.D.; Aggarwal, A.; Lal, A.A.; de la Cruz, V.F.; McCutchan, T.; Nash, T.E.
 J. Exp. Med. 167, 109-118, 1988
 A;Title: Antigenic variation of a cysteine-rich protein in Giardia lamblia.
 A;Reference number: S00530; MUID:88089405; PMID:3335828
 A;Accession: S00530
 A;Molecule type: DNA
 A;Residues: 1154-1409, 'A', 1411-1420, 'K', 1422-1425, 'R', 1427-1481 <ADA3>
 A;Cross-references: EMBL:X06741; NID:g93355; PID:g929603
 R;Yang, Y.; Adam, R.D.
 Nucleic Acids Res. 22, 2102-2108, 1994
 A;Title: Allele-specific expression of a variant-specific surface protein (VSP) of Giardia
 A;Reference number: S48056; MUID:94301794; PMID:8029018
 A;Accession: S48056
 A;Molecule type: DNA
 A;Residues: 1-56 <VAN>
 A;Cross-references: EMBL:L25059
 A;Experimental source: trophozoites WBA6
 A;Note: the source is designated as Giardia intestinalis
 C;Comment: This translation was produced by PIR staff from information provided by the a
 C;Genetics:
 A;Gene: VSPA6
 C;Keywords: surface antigen; tandem repeat

Query Match 88.2%; Score 30; DB 2; Length 1766;
 Best Local Similarity 80.0%; Pred. No. 8.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||
 1504 CHATC 1508

Db

RESULT 48
 B96981
 hypothetical protein CAC0660 [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: B96981
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: B96981
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-67 <KUR>
 A;Cross-references: UNIPROT:Q971A2; GB:AE001437; PIDN:AAK78637.1; PID:g15023535; GSPDB:G
 A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC0660

Query Match 85.3%; Score 29; DB 2; Length 67;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||
 21 CHCIC 25

RESULT 49

T27516
 hypothetical protein ZC334.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T27516
 R;McLay, K.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z20381
 A;Accession: T27516
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-120 <WIL>
 A;Cross-references: UNIPROT:Q9XUI8; EMBL:Z82082; PIDN:CAB04963.1; GSPDB:GN00019; CESP:ZC
 A;Experimental source: clone ZC334
 C;Genetics:
 A;Gene: CESP:ZC334.2
 A;Map position: 1
 A;Introns: 90/1

Query Match 85.3%; Score 29; DB 2; Length 120;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||
 80 CHGIC 84

RESULT 50

Q0EC30
 prelin peptidase dependent protein B precursor - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 31-Mar-1988 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: B65065; C24137
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: B65065
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-187 <BLAT>
 A;Cross-references: UNIPROT:P08371; GB:AE000366; GB:U00096; NID:g1789185; PIDN:AACT5864.
 A;Experimental source: strain K-12, substrain MG1655
 R;Finch, P.W.; Wilson, R.E.; Brown, K.; Hickson, I.D.; Tomkinson, A.E.; Emmerson, P.T.
 Nucleic Acids Res. 14, 4437-4451, 1986
 A;Title: Complete nucleotide sequence of the Escherichia coli recC gene and of the thyA-
 A;Reference number: A93625; MUID:86232583; PMID:3520484
 A;Accession: C24137
 A;Molecule type: DNA
 A;Residues: 'M'PCSPRCWGQVLSNQFTIGLCATLARSNERPDTFACFLWPAQVRMGRAYSLOKLNGRVVAGGFAVGKTPALS;
 A;Cross-references: GB:X03966; NID:g42684; PIDN:CAA27601.1; PID:g42686
 C;Genetics:
 A;Gene: ppdB
 A;Map position: 61 min
 C;Superfamily: prepilin peptidase dependent protein B precursor

Query Match 85.3%; Score 29; DB 1; Length 187;
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||
 68 CHGIC 72

```

RESULT 51
D85934
prepilin peptidase dependent protein B [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85934
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <STO>
A:Cross-references: UNIPROT:Q8X6M2; GB:AE005174; NID:gl2517310; PIDN:AAG57936.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain BDL933
C:Genetics:
A:Gene: pdpB
C:Superfamily: prepilin peptidase dependent protein B precursor

Query Match      85.3%; Score 29; DB 2; Length 187;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5      |||
Db      68 CHGIC 72

RESULT 52
B98089
prepilin peptidase dependent protein B [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: B98089
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehli, K.; Yokoyama, K.; Han, C.G.
gaewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B98089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <RAY>
A:Cross-references: UNIPROT:Q8X6M2; GB:BA000007; PIDN:BA037105.1; PID:gl3363154; GSPDB:G
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: ECe3682
C:Superfamily: prepilin peptidase dependent protein B precursor

Query Match      85.3%; Score 29; DB 2; Length 187;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5      |||
Db      68 CHGIC 72

RESULT 53
G71343
hypothetical protein TP0284 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: G71343
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876

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A:Accession: G71343
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-219 <COI>
A:Cross-references: UNIPROT:O83308; GB:AE001209; GB:AE000520; NID:g3322547; PIDN:AAC6528
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0284
C:Superfamily: syphilis spirochete hypothetical protein TP0284

Query Match      85.3%; Score 29; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5      |||
Db      76 CHQVC 80

RESULT 54
A82147
ABC transporter, ATP-binding protein VC1883 [imported] - Vibrio cholerae (strain N16961
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82147
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: A82147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-228 <HEI>
A:Cross-references: UNIPROT:P57066; GB:AE004263; GB:AE003852; NID:g9656399; PIDN:AAF9503
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1883
A:Map position: 1
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match      85.3%; Score 29; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CHAVC 5      |||
Db      7 CHQVC 11

RESULT 55
S76342
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76342
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <KAN>
A:Cross-references: UNIPROT:O57208; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA1019-
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Mg2+-transporting ATPase

Query Match      85.3%; Score 29; DB 2; Length 234;

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Best Local Similarity 80.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 149 CHLVC 153

RESULT 56
F72426
iron-sulfur cluster-binding protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004
C:Accession: F72426
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72426
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-261 <ARN>
A:Cross-references: UNIPROT:Q9WXQ6; GB:AE001691; GB:AE000512; NID:g4980517; PIDN:AAD3514
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0049
C:Superfamily: ferredoxin 2(4Fe-4S) homology

Query Match 85.3%; Score 29; DB 2; Length 261;
Best Local Similarity 80.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 245 CHEVC 249

RESULT 57
T17632
hypothetical protein al41L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17632
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: T17632
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-265 <GRA>
A:Cross-references: UNIPROT:Q84461; EMBL:U42580; NID:g4028896; PIDN:AAC96509.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Note: al41L

Query Match 85.3%; Score 29; DB 2; Length 265;
Best Local Similarity 60.0%; Pred. No. 3.4e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 256 CHGIC 260

RESULT 58
T52387
hypothetical protein MW12.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52387
R:Kaneko, T.; Kato, T.; Sato, S.; Nakamura, Y.; Asamizu, E.; Tabata, S.

submitted to the EMBL Data Library, September 1999
A:Reference number: Z26062
A:Accession: T52387
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-307 <KAN>
A:Cross-references: UNIPROT:Q9LJN7; EMBL:AP000417; PIDN:BA02544.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 3

Query Match 85.3%; Score 29; DB 2; Length 307;
Best Local Similarity 60.0%; Pred. No. 3.7e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 41 CHGIC 45

RESULT 59
I40700
type II site-specific deoxyribonuclease (EC 3.1.21.4) Cfr9I - Citrobacter freundii
C:Species: Citrobacter freundii
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40700; S37179
R:Lubys, A.; Menkevicius, S.; Timinskas, A.; Butkus, V.; Janulaitis, A.
Gene 141, 85-89, 1994
A:Title: Cloning and analysis of translational control for genes encoding the Cfr9I reest
A:Reference number: I40699; MUID:94215893; PMID:8163180
A:Accession: I40700
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-330 <RES>
A:Cross-references: UNIPROT:Q60132; EMBL:X74517; NID:g402178; PIDN:CAAS2628.1; PID:g4021
C:Genetics:
A:Gene: cfr9IR
C:Keywords: hydrolase

Query Match 85.3%; Score 29; DB 2; Length 330;
Best Local Similarity 80.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 131 CHAFC 135

RESULT 60
A64378
hypothetical protein MJ0625 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: A64378
R:Buit, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
Reich, C.J.; Overbeek, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: A64378
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-336 <BUL>
A:Cross-references: UNIPROT:Q58042; GB:U67510; NID:g1591325; PIDN:AAB98625.1;
C:Genetics:
A:Map position: FOR553608-554618
C:Superfamily: ATP-binding protein PAB1945

Query Match 85.3%; Score 29; DB 2; Length 336;
Best Local Similarity 60.0%; Pred. No. 4e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

A:Molecule type: DNA
A:Residues: 1-416 <STO>
A:Cross-references: UNIPROT:Q9HU99; GB:AE004921; GB:AE004091; NID:g9951372; PIDN:AAG0846
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5084

Query Match 85.3%; Score 29; DB 2; Length 416;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||| |
Db 197 CHAFC 201

RESULT 66
AC0809
xanthosine permease [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain xanthosine permease [imported])
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0809
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R.; Parkhill, J.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; et al.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07653.1; PID:g16503640; GSPDB:GN00176
C:Genetics:
A:Gene: STY2657

Query Match 85.3%; Score 29; DB 2; Length 418;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||| |
Db 75 CHLVC 79

RESULT 67
E65014
xanthosine permease - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: E65014
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65014
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-418 <BLAT>
A:Cross-references: UNIPROT:P45562; GB:AE000328; GB:U00096; NID:g2367135; PIDN:AAC75459
A:Experimental source: strain K-12, substrain MGL655
C:Genetics:
A:Gene: xapB

Query Match 85.3%; Score 29; DB 2; Length 418;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||| |

Db 75 CHLVC 79

RESULT 68
T52320
10-deacetyltransferase [imported] - Taxus cuspidata
C:Species: Taxus cuspidata
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52320
R:Walker, K.; Croteau, R.
Proc. Natl. Acad. Sci. U.S.A. 97, 583-587, 2000
A:Title: Molecular cloning of a 10-deacetyltransferase cDNA from Taxus canadensis
A:Reference number: Z26035
A:Accession: T52320
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-440 <WAL>
A:Cross-references: UNIPROT:Q9M6E2; EMBL:AF193765; PIDN:AAF27621.1
C:Genetics:
A:Gene: DBAT

Query Match 85.3%; Score 29; DB 2; Length 440;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||| |
Db 161 CHGIC 165

RESULT 69
T00918
hypothetical protein F21B7.32 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00918
R:Shinn, P.; Buehler, E.; Dewar, K.; Peng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conzelmann, A.; Ecker, J.R.
submitted to the EMBL Data Library, January 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A:Reference number: Z14208
A:Accession: T00918
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <SHI>
A:Cross-references: UNIPROT:Q9LR83; EMBL:AC002560; NID:g2618677; PID:g2809263; GSPDB:GNO019
C:Genetics:
A:Gene: ATSP:F21B7.32
A:Map position: 1

Query Match 85.3%; Score 29; DB 2; Length 461;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
||| |
Db 176 CHGIC 180

RESULT 70
T20537
hypothetical protein F07A5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20537
R:Wilkinson, J.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19288
A:Accession: T20537
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-590 <WIL>
A:Cross-references: UNIPROT:Q19140; EMBL:Z72506; PIDN:CAA96619.1; GSPDB:GN00019; CESP:F0

A;Experimental source: clone F07A5

C;Genetics:

A;Gene: CESP:F07A5.3

A;Map position: 1

A;Introns: 42/3; 101/2; 151/3; 185/2; 208/3; 240/3; 290/1; 333/2; 370/2; 462/3; 487/2

Query Match 85.3%; Score 29; DB 2; Length 590;

Best Local Similarity 80.0%; Pred. No. 5.9e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 389 CHACC 393

RESULT 71

JC7361

follitropin receptor precursor - newt

N;Alternate names: follicle-stimulating hormone receptor

C;Species: Cynops pyrrhogaster (newt)

C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004

C;Accession: JC7361

R;Nakayama, Y.; Yamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, S.

Biochem. Biophys. Res. Commun. 275, 121-128, 2000

A;Title: Molecular cloning, functional characterization, and gene expression of a follicle-stimulating hormone receptor

A;Reference number: JC7361

A;Contents: testis

A;Accession: JC7361

A;Molecule type: mRNA

A;Residues: 1-696 <NA>

A;Cross-references: UNIPROT:Q9DGF5; DBJ:AB005587

C;Comment: This protein, containing seven transmembrane domains and a large glycosylated extracellular domain, is a member of the G-protein-coupled receptor family. This receptor has a common signal transduction pathway in and thyroid stimulating hormone. This receptor has a common signal transduction pathway in and thyroid stimulating hormone.

C;Genetics:

A;Gene: fsh-r

C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h

C;Keywords: disulfide bond; glycolysis; glycoprotein; hormone receptor; testis; transmem

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-696/Product: follicle-stimulating hormone receptor #status predicted <MAT>

F;18-359/Domain: extracellular #status predicted <EXT>

F;370-389/Domain: transmembrane #status predicted <TM1>

F;402-424/Domain: transmembrane #status predicted <TM2>

F;447-468/Domain: transmembrane #status predicted <TM3>

F;489-511/Domain: transmembrane #status predicted <TM4>

F;532-553/Domain: transmembrane #status predicted <TM5>

F;577-600/Domain: transmembrane #status predicted <TM6>

F;612-633/Domain: transmembrane #status predicted <TM7>

F;46,190,198,267,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.3%; Score 29; DB 2; Length 696;

Best Local Similarity 80.0%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 18 CHPVC 22

RESULT 72

T20635

hypothetical protein F09B9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20635

R;Kershaw, J.

submitted to the EMBL Data Library, June 1995

A;Reference number: Z19303

A;Accession: T20635

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-710 <WIL>

A;Cross-references: UNIPROT:Q19239; EMBL:Z49887; PIDN:CAA90058.1; GSPDB:GN00028; CESP:FO

A;Experimental source: clone F09B9

C;Genetics:

A;Gene: CESP:F09B9.1

A;Map position: X

A;Introns: 82/1; 196/2; 379/1; 626/3; 655/2

C;Superfamily: Caenorhabditis elegans hypothetical protein F09B9.1

Query Match 85.3%; Score 29; DB 2; Length 710;

Best Local Similarity 80.0%; Pred. No. 6.8e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 177 CHAYC 181

RESULT 73

T39715

probable transcription regulator, phd finger protein - fission yeast (Schizosaccharomyces

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T39715

R;Beck, A.; Reinhardt, R.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, September 1998

A;Reference number: Z21872

A;Accession: T39715

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-767 <BEC>

A;Cross-references: UNIPROT:Q74759; EMBL:AL031739; PIDN:CAA21075.1; GSPDB:GN00067; SPDB:1

A;Experimental source: strain 972h; cosmid c17D11

C;Genetics:

A;Gene: SPDB:SPBC17D11.04C

A;Map position: 2

Query Match 85.3%; Score 29; DB 2; Length 767;

Best Local Similarity 60.0%; Pred. No. 7.2e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 270 CHTIC 274

RESULT 74

D96503

protein F9C16.9 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: D96503

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D96503

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-946 <STO>

A;Cross-references: UNIPROT:Q9LP09; GB:AE005173; NID:g8778679; PIDN:AAF79687.1; GSPDB:GN1

C;Genetics:

A;Gene: F9C16.9

A;Map position: 1

Query Match 85.3%; Score 29; DB 2; Length 946;

Best Local Similarity 80.0%; Pred. No. 8.3e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 96 CHVC 100

RESULT 75
JC4387
epidermal growth factor receptor homolog precursor - rat
N:Alternate names: ErbB3 protein; HER3 protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
C/Accession: JC4387
R:Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.
Gene 165, 279-284, 1995
A:Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.
A:Reference number: JC4387; MUID:96096535; PMID:8522190
A/Accession: JC4387
A/Molecule type: mRNA
A/Residues: 1-1339 <HEL>
A/Cross-references: GB:U293339; NID:g915309; PID:g915390
A:Experimental source: liver
A:Note: The authors translated the codon AAC for residue 369 as Thr and GTT for residue 370.
C:Comment: This protein is a functional heregulin receptor that transduces signals to the cell.
C/Genetics:
A:Gene: ErbB3
C:Superfamily: protein kinase homology
C:Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:1-1339/Product: epidermal growth factor homolog #status predicted <WAT>
F:20-1339/Product: transmembrane #status predicted <TMM>
F:640-659/Domain: protein kinase homology <KIN>
F:705-970/Domain: protein kinase homology <KIN>
F:713-721/Region: protein kinase ATP-binding motif
F:939, 1051, 1156, 1194, 1196, 1219, 1257, 1259, 1273, 1286, 1325/Binding site: phosphate (Tyr) (C)
Query Match 85.3%; Score 29; DB 2; Length 1339;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 186 CHEVC 190

RESULT 76
A36223
kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human
C:Species: Homo sapiens (man)
C>Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C/Accession: A36223; I59164
R:Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989
A:Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor gene family.
A:Reference number: A36223; MUID:90083234; PMID:2687875
A/Accession: A36223
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1342 <KRA>
A/Cross-references: UNIPROT:P21860; GB:M29366
R:Plowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G.J.
Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A:Title: Molecular cloning and expression of another epidermal growth factor receptor-related protein.
A:Reference number: I59164; MUID:90311312; PMID:2164210
A/Accession: I59164
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-559, 'G', '561-957', 'F', '959-1063', 'G', '1065-1342' <RES>
A/Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841
C/Genetics:
A:Gene: GDB:ERBB3; HER3
A/Cross-references: GDB:119880; OMIM:190151
A/Map position: 12q13-12q13
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

C:Keywords: ATP; phosphotransferase
F:707-972/Domain: protein kinase homology <KIN>
F:715-723/Region: protein kinase ATP-binding motif

Query Match 85.3%; Score 29; DB 2; Length 1342;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 186 CHEVC 190

RESULT 77
T00209
MEGF8 protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C/Accession: T00209
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A/Accession: T00209
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1737 <NAK>
A/Cross-references: EMBL:AB011541; NID:G3449307; PIDN:BAA32469.1; PID:G3449308
A:Experimental source: brain; clone HG1392
C/Genetics:
A:Gene: MEGF8
A/Map position: 19q12

Query Match 85.3%; Score 29; DB 2; Length 1737;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1194 CHAF 1198

RESULT 78
T18472
hypothetical protein C0440c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18472
R:Lawson, D.; Bowman, S.; Barrell, B.
Submitted to the EMBL Data Library, November 1998
A:Reference number: Z18937
A/Accession: T18472
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2269 <LAW>
A/Cross-references: UNIPROT:O77360; EMBL:AL008970; NID:e1407852; PID:e1332566; PIDN:CAA1
C/Genetics:
A:Gene: C0440c
A/Map position: 3

Query Match 85.3%; Score 29; DB 2; Length 2269;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||
Db 1007 CHGC 1011

RESULT 79
T38057
hypothetical protein SPAC1E11.02 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38057
R;Skelton, J.; Churcher, C.M.; Barrrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21751
A:Accession: T38057
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-110 <SKE>
A:Cross-references: UNIPROT:O13886; EMBL:Z98599; PIDN:CAB11249.2; GSPDB:GN000066; SPDB:SP
A:Experimental source: strain 972h-; cosmid c1811
C:Genetics:
A:Gene: SPDB:SPAC1E11.02
A:Map position: 1
A:Introns: 33/3; 43/2; 54/3; 58/2

Query Match 82.4%; Score 28; DB 2; Length 110;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
DB 55 CHAKC 59

RESULT 80

T17545

Hypothetical protein a55L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T17545

R;Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T17545

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-131 <GRA>

A:Cross-references: UNIPROT:Q99390; EMBL:U42580; NID:G4028896; PIDN:AAC96423.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Gene: a55L

Query Match

Best Local Similarity 82.4%; Score 28; DB 2; Length 131;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||
DB 99 CHHVC 103

RESULT 81

T23781

Hypothetical protein M163.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T23781

R;Percy, C.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19798

A:Accession: T23781

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-157 <WIL>

A:Cross-references: UNIPROT:Q93904; EMBL:Z79603; PIDN:CAB01895.1; GSPDB:GN000028; CESP:M1

A:Experimental source: clone M163

C:Genetics:

A:Gene: CESP:M163.6

A:Map position: X

A:Introns: 64/3; 78/3; 99/3; 109/1; 136/1

Query Match

82.4%; Score 28; DB 2; Length 157;

Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CHAVC 5
|||
DB 29 CHHVC 33

RESULT 82

I46204

Interferon-alpha - dog

C:Species: Canis lupus familiaris (dog)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46204; I46205

R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.

J. Interferon Res. 7, 173-183, 1987

A:Title: Structure and expression in Escherichia coli of canine interferon-alpha genes.

A:Reference number: I46204; MUID:87281775; PMID:3039013

A:Accession: I46204

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-187 <HIM>

A:Cross-references: UNIPROT:P81255; GB:M28624; NID:G163973; PIDN:AAA30850.1; PID:G163974

A:Accession: I46205

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-187 <H12>

A:Cross-references: GB:M28625; NID:G163975; PIDN:AAA30851.1; PID:G163976

C:Genetics:

A:Gene: IFN-alpha

C:Superfamily: interferon alpha

Query Match

Best Local Similarity 82.4%; Score 28; DB 2; Length 187;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
||:|
DB 16 CHSLC 20

RESULT 83

I46206

Interferon-alpha - dog

C:Species: Canis lupus familiaris (dog)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46206

R;Himmler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.

J. Interferon Res. 7, 173-183, 1987

A:Title: Structure and expression in Escherichia coli of canine interferon-alpha genes.

A:Reference number: I46204; MUID:87281775; PMID:3039013

A:Accession: I46206

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-187 <HIM>

A:Cross-references: UNIPROT:O97945; GB:M28626; NID:G163977; PIDN:AAA30852.1; PID:G163978

C:Genetics:

A:Gene: IFN-alpha

C:Superfamily: interferon alpha

Query Match

Best Local Similarity 82.4%; Score 28; DB 2; Length 187;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
||:|
DB 16 CHSLC 20

RESULT 84

AC0359

Probable membrane protein YPO2952 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
A;Accession: AC0359
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-227 <KUR>
A;Cross-references: UNIPROT:Q8ZCM9; GB:AL590842; PIDN:CAC92198.1; PID:G15980910; GSPDB:G15980910
C;Genetics:
A;Gene: YPO2952

Query Match 82.4%; Score 28; DB 2; Length 227;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:
Db 58 CHQIC 62

RESULT 85
T43487
hypothetical protein DKFZp434B217.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
A;Accession: T43487
R;Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, December 1999
A;Reference number: Z22514
A;Accession: T43487
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-230 <ARA>
A;Cross-references: UNIPROT:Q9UF79; EMBL:AL133566
A;Experimental source: adult testis; clone DKFZp434B217
C;Genetics:
A;Note: DKFZp434B217.1
C;Superfamily: kexin; subtilisin homology

Query Match 82.4%; Score 28; DB 2; Length 230;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:
Db 127 CHASC 131

RESULT 86
C44954
fumarate reductase (EC 1.3.99.1) iron-sulfur protein - Wolinella succinogenes
N;Alternate names: fumarate reductase chain B
C;Species: Wolinella succinogenes
C;Date: 03-Jun-1993 #sequence_revision 19-Jul-1996 #text_change 12-Jul-2004
A;Accession: C44954; S10166
R;Lauterbach, F.; Koertner, C.; Albracht, S.P.J.; Unden, G.; Kroeger, A. Arch. Microbiol. 154, 386-393, 1990
A;Title: The fumarate reductase operon of Wolinella succinogenes. Sequence and expression
A;Reference number: A44954; MUID:91058386; PMID:2244791
A;Accession: C44954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-239 <LAU>
A;Cross-references: UNIPROT:P17596; GB:X51509; NID:948511; PIDN:CAA35876.1; PID:G48514
R;Koertner, C.; Lauterbach, F.; Tripiet, D.; Unden, G.; Kroeger, A. Mol. Microbiol. 4, 855-860, 1990
A;Title: Wolinella succinogenes fumarate reductase contains a dihaem cytochrome b.
A;Reference number: S10164; MUID:90355847; PMID:2388563

A;Accession: S10166
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-239 <KOE>
A;Cross-references: EMBL:X51509; NID:948511; PIDN:CAA35876.1; PID:G48514
C;Genetics:
A;Gene: frdB
A;Complex: part of an enzyme complex containing a heterotrimer (flavoprotein, iron-sulfur)
C;Function:
A;Description: catalyzes the oxidation of succinate to fumarate and transfers its reduced f the complex together with the iron sulfur subunit
C;Superfamily: fumarate reductase/succinate dehydrogenase (ubiquinone), iron-sulfur prot;
C;Keywords: 2Fe-2S; 3Fe-4S; 4Fe-4S; heterotrimer; iron-sulfur protein; metalloprotein;
F;38-78/Domain: ferredoxin [2Fe-2S] homology <PFR1>
F;144-226/Domain: ferredoxin 2[4Fe-4S] homology <PFR2>
F;57,62,65,77/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
F;151,154,157,218/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;161,208,214/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 82.4%; Score 28; DB 1; Length 239;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:
Db 214 CHDVC 218

RESULT 87
D86266
hypothetical protein F3F19.22 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A;Accession: D86266
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <STO>
A;Cross-references: UNIPROT:Q9SAF3; GB:AE005172; NID:94850408; PIDN:AAD31078.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.40; RING finger homology

Query Match 82.4%; Score 28; DB 2; Length 260;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:
Db 178 CHSMC 182

RESULT 88
AG0041
L-rhamnose operon transcription activator rhaR [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
A;Accession: AG0041
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AG0041
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-290 <KUR>
 A;Cross-references: UNIPROT:Q821Z3; GB:AL590842; PIDN:CAC89194.1; PID:g15978433; GSPDB:G
 C;Genetics:
 A;Gene: rhaR
 C;Superfamily: hypothetical protein b2382

Query Match 82.4%; Score 28; DB 2; Length 290;
 Best Local Similarity 80.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
 |||
 Db 231 CHAKC 235

RESULT 89

JE0174
 frizzled protein-2 - human
 C;Species: Homo sapiens (man)
 C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
 C;Accession: JE0174
 R;Hu, B.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
 Biochem. Biophys. Res. Commun. 247, 287-293, 1998
 A;Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
 A;Reference number: JE0174; MUID:98308108; PMID:9642118
 A;Accession: JE0174
 A;Molecule type: mRNA
 A;Residues: 1-295 <HUA>
 A;Cross-references: UNIPROT:Q9HAP5
 C;Genetics:
 A;Map position: 4q

Query Match 82.4%; Score 28; DB 2; Length 295;
 Best Local Similarity 60.0%; Pred. No. 5.4e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 |||
 Db 114 CHSLC 118

RESULT 90

T22393
 hypothetical protein F49A5.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T22393

R;Mortimore, B.
 submitted to the EMBL Data Library, November 1996

A;Reference number: Z19560
 A;Accession: T22393
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-308 <MIL>
 A;Cross-references: UNIPROT:O45530; EMBL:Z81542; PIDN:CAB04415.1; GSPDB:GN00023; CESP:F4
 A;Experimental source: clone F49A5
 C;Genetics:
 A;Gene: CESP:F49A5.4
 A;Map position: 5
 A;Introns: 46/1; 95/3; 144/1; 187/1

Query Match 82.4%; Score 28; DB 2; Length 308;
 Best Local Similarity 80.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
 |||
 Db 297 CHPVC 301

RESULT 91

JC7096
 leukotriene B4 receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: JC7096
 R;Toda, A.; Yokomizo, T.; Masuda, K.; Nakao, A.; Izumi, T.; Shimizu, T.
 Biochem. Biophys. Res. Commun. 262, 806-812, 1999
 A;Title: Cloning and characterization of rat leukotriene B4 receptor.
 A;Reference number: JC7096; MUID:99400454; PMID:10471406
 A;Accession: JC7096
 A;Molecule type: mRNA
 A;Residues: 1-351 <TOD>
 A;Cross-references: UNIPROT:Q9R0Q2; DBJ:AB025230; NID:G5921091; PIDN:BAA84578.1; PID:G5:

C;Genetics:
 A;Gene: blt
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: disulfide bond; glycoprotein; receptor; signal transduction; transmembrane p

Query Match 82.4%; Score 28; DB 2; Length 351;
 Best Local Similarity 80.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
 |||
 Db 95 CHYVC 99

RESULT 92

I38429
 connexin40 - human
 C;Species: Homo sapiens (man)
 C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
 C;Accession: I38429
 R;Kanter, H.L.; Saffitz, J.E.; Beyer, E.C.
 J. Mol. Cell. Cardiol. 26, 861-868, 1994
 A;Title: Molecular cloning of two human cardiac gap junction proteins, connexin40 and co
 A;Reference number: I38429; MUID:95055780; PMID:7966354
 A;Accession: I38429
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-358 <RES>
 A;Cross-references: EMBL:U03486; NID:G416327; PIDN:AAA60457.1; PID:G416328
 C;Superfamily: gap junction protein

Query Match 82.4%; Score 28; DB 2; Length 358;
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
 |||
 Db 61 CHNVC 65

RESULT 93

A49107
 alcohol dehydrogenase (EC 1.1.1.1) I - deer mouse
 N;Alternate names: alcohol dehydrogenase 1
 C;Species: Peromyscus maniculatus (deer mouse)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: A49107
 R;Zheng, Y.W.; Bey, M.; Liu, H.; Felder, M.R.
 J. Biol. Chem. 268, 24933-24939, 1993
 A;Title: Molecular basis of the alcohol dehydrogenase-negative deer mouse. Evidence for
 A;Reference number: A49107; MUID:94043358; PMID:8227055
 A;Accession: A49107
 A;Molecule type: mRNA
 A;Residues: 1-375 <ZHE>

A;Cross-references: UNIPROT:P41680; GB:I15703; NID:G416387; PIDN:AAA40591.1; PID:G416388
 C;Comment: The class I alcohol dehydrogenases are pyrazole-sensitive and have a high acti
 C;Genetics:

A;Gene: Adh-1
 C;Complex: homodimer (A2 isozyme)
 C;Function:
 A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes and
 A;Pathway: alcohol degradation
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 F;2-375/Product: alcohol dehydrogenase alpha #status predicted <MAT>
 F;32-366/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F;195-224/Region: beta-alpha-beta NAD nucleotide-binding fold
 F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
 F;47,68,175/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
 F;98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 82.4%; Score 28; DB 1; Length 375;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||
 Db 283 CHASC 287

RESULT 94
 S07825
 hypothetical protein 2 - fruit fly (Drosophila melanogaster) transposon FB
 C;Species: Drosophila melanogaster
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C;Accession: S07825
 R;Templeton, N.S.; Potter, S.S.
 EMBO J. 8, 1887-1894, 1989
 A;Title: Complete foldback transposable elements encode a novel protein found in Drosophila
 A;Reference number: S07824; MUID:89356666; PMID:2548860
 A;Accession: S07825
 A;Molecule type: DNA
 A;Residues: 1-403 <TEM>
 A;Cross-references: UNIPROT:P16320; EMBL:X15469; NID:G7962; PIDN:CAA33497.1; PID:G7964
 C;Genetics:
 A;Gene: FlyBase:NOP
 A;Cross-references: FlyBase:FBgn0002949
 C;Keywords: nucleus

Query Match 82.4%; Score 28; DB 2; Length 403;
 Best Local Similarity 60.0%; Pred. No. 6.7e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||
 Db 336 CHRIC 340

RESULT 95
 S44909
 ZK686.4 protein - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S44909
 R;Du, Z.
 submitted to the EMBL Data Library, June 1993
 A;Description: Sequence of the C. elegans cosmid ZK686.
 A;Reference number: S44909
 A;Accession: S44909
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-407 <DUZ>
 A;Cross-references: UNIPROT:P34670; EMBL:L17337; NID:G304345; PID:G304346
 C;Genetics:
 A;Intron: 156/3; 190/1; 212/3; 333/1
 C;Keywords: DNA binding; nucleus

Query Match 82.4%; Score 28; DB 2; Length 407;
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||
 Db 50 CHPVC 54

RESULT 96

B36067

thyroid hormone receptor alpha-B - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 09-Jul-2004

C;Accession: B36067

R;Yaoita, Y.; Shi, Y.; Brown, D.D.

Proc. Natl. Acad. Sci. U.S.A. 87, 7090-7094, 1990

A;Title: Xenopus laevis alpha and beta thyroid hormone receptors.

A;Reference number: A36067; MUID:90384953; PMID:2402492

A;Accession: B36067

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-418 <YAO>

C;Cross-references: UNIPROT:P18115; GB:M35344; NID:G214831; PIDN:AAA49970.1; PID:G214832

C;Superfamily: thyroid hormone receptor; erba transforming protein homology

C;Keywords: DNA binding; nucleus; thyroid hormone receptor; transcription regulation; z; zi

F;53-335/Domain: erba transforming protein homology <ERBA>

F;61-81/Region: zinc finger

F;99-123/Region: zinc finger

Query Match 82.4%; Score 28; DB 2; Length 418;

Best Local Similarity 80.0%; Pred. No. 6.9e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

|||

Db 388 CHASC 392

RESULT 97

A55089

vasopressin V3 receptor - human

N;Alternate names: vasopressin receptor V-1B

C;Species: Homo sapiens (man)

C;Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A55089; S51011

R;Sugimoto, T.; Saito, M.; Mochizuki, S.; Watanabe, Y.; Hashimoto, S.; Kawashima, H.

J. Biol. Chem. 269, 27088-27092, 1994

A;Title: Molecular cloning and functional expression of a cDNA encoding the human V-1b

A;Reference number: A55089; MUID:95014580; PMID:7929452

A;Accession: A55089

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-424 <SUG>

A;Cross-references: UNIPROT:P47901; GB:D31833; NID:G563981; PIDN:BA06621.1; PID:G563982

R;de Keyser, Y.; Auzan, C.; Lenne, P.; Beldjord, C.; Thibonnier, M.; Bertagna, X.; Claus

FEBS Lett. 356, 215-220, 1994

A;Title: Cloning and characterization of the human V3 pituitary vasopressin receptor.

A;Reference number: S51011; MUID:95104418; PMID:7805841

A;Accession: S51011

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-424 <DBK>

A;Cross-references: EMBL:L37112; NID:G791151; PIDN:AAA65687.1; PID:G722622

A;Note: the sequence from Fig. 2A is inconsistent with that from Fig. 1 in having 371-11

C;Superfamily: oxytocin receptor

C;Keywords: transmembrane protein

Query Match 82.4%; Score 28; DB 2; Length 424;

Best Local Similarity 60.0%; Pred. No. 7e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CHAVC 5

|||

Db 223 CHRIC 227

RESULT 98

T03152
transcription control protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03152
R;Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: T14840; MUID:97404659; PMID:9261371
A;Accession: T03152
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-436 <ENS>
A;Cross-references: UNIPROT:O36407; EMBL:AF005370; NID:G2337967; PIDN:AAC58104.1; PID:9261371
C;Genetics:
A;Introns: 17/1
C;Superfamily: eaimiri herpesvirus 52K immediate-early protein

Query Match 82.4%; Score 28; DB 2; Length 436;
Best Local Similarity 60.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
||| :|
Db 327 CHIC 331

RESULT 99

JQ0507
adenosylmethionine-8-amino-7-oxononanoate transaminase (EC 2.6.1.62) - Bacillus sphaericus
N;Alternate names: 7,8-diaminononanoate aminotransferase DAPA aminotransferase; adenosyl
C;Species: Bacillus sphaericus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ0507
R;Gloeckler, R.; Ohsawa, I.; Speck, D.; Ledoux, C.; Bernard, S.; Zinsius, M.; Villevall, Gene 87, 63-70, 1990
A;Title: Cloning and characterization of the Bacillus sphaericus genes controlling the
A;Reference number: JQ0506; MUID:90236299; PMID:2110099
A;Accession: JQ0507
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-455 <GLO>
A;Cross-references: UNIPROT:P22805; GB:M29292; NID:G142587; PIDN:AAB02325.1; PID:G142589
A;Experimental source: strain IFO3525
C;Comment: The enzyme catalyzes the condensation of 8-amino-7-oxononanoate and S-adenosyl
C;Genetics:
A;Gene: bicaA
A;Start codon: GTG
C;Superfamily: beta-alanine-pyruvate transaminase
C;Keywords: aminotransferase; biotin biosynthesis; phosphoprotein; pyridoxal phosphate
F;285/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 82.4%; Score 28; DB 1; Length 455;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
||| :|
Db 197 CHAC 201

RESULT 100

S58882
protein kinase Cds1 (EC 2.7.1.1-) [validated] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S58882; S71846; T41204; T52473
R;Murakami, H.; Okayama, H.
Nature 374, 817-819, 1995
A;Title: A kinase from fission yeast responsible for blocking mitosis in S phase.
A;Reference number: S58882; MUID:95240713; PMID:7723827

A;Accession: S58882
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-460 <MUR1>
A;Cross-references: UNIPROT:Q09170; EMBL:X85040; NID:G794146
R;Murakami, H.
submitted to the EMBL Data Library, March 1995
A;Reference number: S71846

A;Accession: S71846
A;Molecule type: mRNA
A;Residues: 1-60, 'G', 62-202, 'I', 204-460 <MUR2>
A;Cross-references: EMBL:X85040; NID:G794146; PIDN:CAAS9410.1; PID:G794147
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21978

A;Accession: T41204
A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-202, 'I', 204-237, 'F', 239-460 <WOO>
A;Cross-references: EMBL:AL109736; NID:G5701956; PIDN:CAB52158.1; PID:G5701966; GSPDB:GN
A;Experimental source: strain 972h(-); cosmid c18B5
R;Lindsay, H.D.; Griffiths, D.J.F.; Edwards, R.J.; Christensen, P.U.; Murray, J.M.; Omar Genes Dev. 12, 382-395, 1998
A;Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoint
A;Reference number: Z26084; MUID:98119835; PMID:9450932

A;Accession: T52473

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-202, 'I', 204-237, 'F', 239-460 <LIN>

A;Cross-references: EMBL:AJ222869; NID:G2689196; PIDN:CAAL1019.1; PID:G2689197
C;Genetics:
A;Gene: SPBC1885.11c; cds1

A;Map position: 3

A;Introns: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2

C;Function:

A;Description: EC 2.7.1.1-; protein kinase Cds1 [validated, MUID:98119835]; is required to
A;Note: Cds1 is phosphorylated and activated by S-phase arrest and activated by DNA dama
C;Superfamily: protein kinase Cds1; kinase interaction domain homology; protein kinase b
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;62-133/Domain: kinase interaction domain homology <KIH>
F;165-433/Domain: protein kinase homology <KIN>
F;173-181/Region: protein kinase ATP-binding motif

Query Match 82.4%; Score 28; DB 2; Length 460;
Best Local Similarity 60.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHAVC 5
||| :|
Db 234 CHEIC 238

Search completed: July 27, 2005, 00:01:48

Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 23:51:00 ; Search time 173 Seconds
(without alignments)

14.800 Million cell updates/sec

Title: US-10-632-678-10

Perfect score: 34

Sequence: 1 CHAVC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	114	2	Q9D974 mus musculus
2	34	100.0	170	2	Q91013 human cytom
3	34	100.0	170	2	Q6SX57 human cytom
4	34	100.0	235	2	Q8SBA1 oryza sativ
5	34	100.0	235	2	Q7XC69 oryza sativ
6	34	100.0	238	2	Q9FPE1 oryza sativ
7	34	100.0	244	2	Q8L3T0 arabidopsis
8	34	100.0	293	2	Q692Q5 citrus tris
9	34	100.0	293	2	Q692Q6 citrus tris
10	34	100.0	293	2	Q692Q7 citrus tris
11	34	100.0	293	2	Q692Q8 citrus tris
12	34	100.0	293	2	Q692Q9 citrus tris
13	34	100.0	293	2	Q692R0 citrus tris
14	34	100.0	293	2	Q692R1 citrus tris
15	34	100.0	293	2	Q692R2 citrus tris
16	34	100.0	381	2	Q8T913 drosophila
17	34	100.0	382	2	Q7X8U8 oryza sativ
18	34	100.0	400	2	Q769C8 psychrobact
19	34	100.0	400	2	Q9L514 psychrobact
20	34	100.0	424	2	Q7FRE7 oryza sativ
21	34	100.0	465	2	Q7QVC3 giardia lam
22	34	100.0	537	2	Q9MZU5 sus scrofa
23	34	100.0	544	2	Q69T84 oryza sativ
24	34	100.0	660	2	Q7QY47 giardia lam
25	34	100.0	3107	2	P87587 citrus tris
26	34	100.0	3115	2	O10467 citrus tris
27	34	100.0	3115	2	Q9IFX0 citrus tris
28	34	100.0	3115	2	Q9WID7 citrus tris
29	34	100.0	3122	2	Q8B3T9 citrus tris
30	34	100.0	3132	2	Q9DTG5 citrus tris
31	34	100.0	5636	2	Q9N9M2 leishmania

ALIGNMENTS

32	33	97.1	75	2	Q74N15	Q74N15 nanoarchaeu
33	33	97.1	168	2	Q6AAV7	Q6AAV7 plasmodi
34	33	97.1	198	2	Q8IBP3	Q8IBP3 plasmodi
35	33	97.1	273	2	Q8Y2B0	Q8Y2B0 taistonis
36	33	97.1	383	2	Q76856	Q76856 dictyosteli
37	33	97.1	397	2	Q993M6	Q993M6 autonomic
38	33	97.1	402	1	VN34_ROTBS	VN34_ROTBS bovine rota
39	33	97.1	402	1	VN34_ROTBS	VN34_ROTBS porcine rot
40	33	97.1	402	2	Q9PY95	Q9PY95 human rotav
41	33	97.1	428	2	Q9MIQ8	Q9MIQ8 arabidopsis
42	33	97.1	665	2	O71159	O71159 kilham rat
43	33	97.1	668	1	VNCS_PAVL3	VNCS_PAVL3 parvovirus
44	33	97.1	672	1	VNCS_MUMIM	VNCS_MUMIM murine minu
45	33	97.1	672	1	VNCS_MUMIV	VNCS_MUMIV murine minu
46	33	97.1	672	1	VNCS_PAVHH	VNCS_PAVHH hamster par
47	33	97.1	672	2	P88899	P88899 kilham rat
48	33	97.1	672	2	Q8JV14	Q8JV14 rat minute
49	33	97.1	672	2	Q8JV16	Q8JV16 rat minute
50	33	97.1	672	2	Q8JV18	Q8JV18 rat minute
51	33	97.1	672	2	Q8JV28	Q8JV28 kilham rat
52	33	97.1	672	2	Q83429	Q83429 mouse parvo
53	33	97.1	721	2	Q84363	Q84363 murine minu
54	33	97.1	721	2	Q84365	Q84365 murine minu
55	33	97.1	815	2	Q6ES22	Q6ES22 oryza sativ
56	33	97.1	929	2	Q7XDU9	Q7XDU9 oryza sativ
57	33	97.1	1092	2	Q6L4D3	Q6L4D3 oryza sativ
58	31	91.2	64	1	SCX1_MESTA	SCX1_MESTA mesobuthus
59	31	91.2	108	2	Q8D488	Q8D488 vibrio vuln
60	31	91.2	116	2	Q7MPR2	Q7MPR2 vibrio vuln
61	31	91.2	118	2	Q8C3T4	Q8C3T4 mus musculus
62	31	91.2	124	2	Q8QY23	Q8QY23 rana tigrin
63	31	91.2	139	2	Q8TXX8	Q8TXX8 methanopyru
64	31	91.2	168	2	Q91019	Q91019 human cytom
65	31	91.2	168	2	Q6SX91	Q6SX91 human cytom
66	31	91.2	168	2	Q6SX88	Q6SX88 human cytom
67	31	91.2	170	2	Q914P6	Q914P6 human cytom
68	31	91.2	170	2	Q914P8	Q914P8 human cytom
69	31	91.2	170	2	Q914P9	Q914P9 human cytom
70	31	91.2	171	1	IR10_HCMVA	IR10_HCMVA human cytom
71	31	91.2	171	2	Q914P7	Q914P7 human cytom
72	31	91.2	171	2	Q69029	Q69029 human cytom
73	31	91.2	171	2	Q6SX75	Q6SX75 human cytom
74	31	91.2	171	2	Q6SX75	Q6SX75 human cytom
75	31	91.2	171	2	Q8XK6	Q8XK6 human cytom
76	31	91.2	222	2	Q7M6G1	Q7M6G1 human cytom
77	31	91.2	222	2	Q8C2H6	Q8C2H6 mus musculus
78	31	91.2	222	2	Q8C2R3	Q8C2R3 mus musculus
79	31	91.2	230	2	Q8WYK4	Q8WYK4 homo sapien
80	31	91.2	232	2	Q8QNP2	Q8QNP2 ectocarpus
81	31	91.2	251	2	Q9FYL9	Q9FYL9 arabidopsis
82	31	91.2	261	2	Q7MU57	Q7MU57 porphyromon
83	31	91.2	272	2	Q9VDN1	Q9VDN1 drosophila
84	31	91.2	279	2	Q8WYK3	Q8WYK3 homo sapien
85	31	91.2	307	1	TVSY_MOUSE	TVSY_MOUSE mus musculus
86	31	91.2	307	1	TVSY_RAT	TVSY_RAT mus musculus
87	31	91.2	307	2	Q9D0H1	Q9D0H1 mus musculus
88	31	91.2	310	2	Q8VDV6	Q8VDV6 mus musculus
89	31	91.2	312	1	TVSY_HUMAN	TVSY_HUMAN drosophila
90	31	91.2	318	2	Q6P0I5	Q6P0I5 brachydanio
91	31	91.2	319	2	Q7ZUI7	Q7ZUI7 brachydanio
92	31	91.2	319	2	Q9DGH5	Q9DGH5 brachydanio
93	31	91.2	373	2	P91501	P91501 caenorhabdi
94	31	91.2	380	2	Q8EED1	Q8EED1 shewanella
95	31	91.2	387	2	Q8XR48	Q8XR48 ralestonia s
96	31	91.2	391	2	Q756V7	Q756V7 ashbya goss
97	31	91.2	404	2	Q6DD86	Q6DD86 xenopus lae
98	31	91.2	447	2	Q8X0Q2	Q8X0Q2 neurospora
99	31	91.2	481	2	Q89GP2	Q89GP2 bradyrhizob
100	31	91.2	502	2	Q7QDB4	Q7QDB4 anopheles g

RESULT 1
 Q9D974 PRELIMINARY; PRT; 114 AA.
 AC Q9D974;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700127D06 product:similar to tissue kallikrein (EC 3.4.21.35), submandibular mGK-2.
 DE library, clone:1700127D06Rik;
 GN Name=1700127D06Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Akawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK007298; BAB24941.1; -;
 DR HSSP; P00756; ISGF.
 DR MEROPS; S01.107; -;
 DR MGD; MGI:1924249; 1700127D06Rik.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 114 AA; 13082 MW; CF6C05A967C47546 CRC64;

 Query Match 100.0%; Score 34; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred.No.70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 35 CHAVC 39

 RESULT 2
 Q91013 PRELIMINARY; PRT; 170 AA.
 AC Q91013;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE TRL10.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TB40E, and 36vuek;
 RX MEDLINE=21635521; PubMed=11773418;
 RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
 RT "Identification of glycoprotein gpRL10 as a structural component of human cytomegalovirus.";
 RL J. Virol. 76:1450-1460(2002).
 DR EMBL; AF432092; AAL27474.1; -;
 DR EMBL; AF432086; AAL27468.1; -;
 DR Pfam; PF06084; Cytomega_TRL10; 1.
 SQ SEQUENCE 170 AA; 18940 MW; B496BE5601E33739 CRC64;

 Query Match 100.0%; Score 34; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred.No.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 59 CHAVC 63

 RESULT 3
 Q6SX57 PRELIMINARY; PRT; 170 AA.
 AC Q6SX57;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE RL10.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.

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OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3157;
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
RA Davison A.J.;
RT "Genetic content of wild-type human cytomegalovirus.";
RL J. Gen. Virol. 85:1301-1312(2004).
DR EMBL; AY446863; AAR31286.1; -.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 170 AA; 18942 MW; 8C851AB8E3473D71 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 59 CHAVC 63

RESULT 4
Q8SBA1 PRELIMINARY; PRT; 235 AA.
AC Q8SBA1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein OSJNBa0042H09.16;
GN Name=OSJNBa0042H09.16;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Heiao J., Zismann V., Blunt S., Pai G.,
RA Varaken S.E., Utkerback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC079874; AAL79784.1; -.
DR Gramene; Q8SBA1; -.
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25948 MW; 11D13F750B1046F7 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 113 CHAVC 117

RESULT 5
Q7XC69 PRELIMINARY; PRT; 235 AA.
AC Q7XC69;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OSJNBa0042H09.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017119; AAP55005.1; -.
DR Gramene; Q7XC69; -.
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25948 MW; 11D13F750B1046F7 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 113 CHAVC 117

RESULT 6
Q9FPE1 PRELIMINARY; PRT; 238 AA.
AC Q9FPE1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein At2g45010 (Fragment).
GN Name=At2g45010;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.W., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Mikanda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327424; AAG42014.1; -.
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
FT NON_TER 238
SQ SEQUENCE 238 AA; 26581 MW; B272FAA3B46A7FB7 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

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Db          106 CHAVC 110
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RESULT 7
Q8L3T0      PRELIMINARY;      PRT;      244 AA.
AC Q8L3T0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein At2g45010.
GN Name=At2g45010.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Peus D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RA thaliana.";
RA Nature 402:761-768 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Lin X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troughan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RA "Full-length messenger RNA sequences greatly improve genome
RA annotation.";
RA Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA Ecker J.R., Theologis A.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY120733; AAM53291.1; -
DR EMBL; AC007659; AAD32834.1; -
DR EMBL; AY087375; AAM64925.1; -
DR EMBL; AK118360; BAC42974.1; -
DR EMBL; BT000360; AAN15679.1; -
DR EMBL; BT000899; AAN41299.1; -
DR PIR; E84885; E84885;
DR InterPro; IPR006461; DUF_A_thal_Cys.
DR Pfam; PF04749; DUF614; 1.
DR TIGRFAMs; TIGR01571; A_thal_Cys_rich; 1.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27264 MW; F03B26523376E272 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 106 CHAVC 110

RESULT 8
Q692Q5      PRELIMINARY;      PRT;      293 AA.
AC Q692Q5;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Irturiga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652915; AAT75285.1; -
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32161 MW; 170A2DC266A948AF CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 118 CHAVC 122

RESULT 9
Q692Q6      PRELIMINARY;      PRT;      293 AA.
AC Q692Q6;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.

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OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652914; AAT75284.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32000 MW; 82B2464AC4E6348 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 10
Q692Q7 PRELIMINARY; PRT; 293 AA.
AC Q692Q7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652913; AAT75283.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32066 MW; 43CCB67B0D6176A9 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 11
Q692Q8 PRELIMINARY; PRT; 293 AA.
AC Q692Q8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";

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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652912; AAT75282.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32131 MW; B530226B67053FDE CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 12
Q692Q9 PRELIMINARY; PRT; 293 AA.
AC Q692Q9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652911; AAT75281.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32746 MW; C85B45D4DFCB7775 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 118 CHAVC 122

RESULT 13
Q692R0 PRELIMINARY; PRT; 293 AA.
AC Q692R0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Iturriga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RA "Molecular analysis of Citrus tristeza virus isolates from Mexico.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY652910; AAT75280.1; -.
FT NON_TER 1
FT NON_TER 293
SQ SEQUENCE 293 AA; 32074 MW; D21D1D6D2A3D7ECC CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;

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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
118 CHAVC 122

RESULT 14

Q692R1 ID Q692R1 PRELIMINARY; PRT; 293 AA.
AC Q692R1;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Icurtiaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RT "Molecular analysis of Citrus tristeza virus isolates from Mexico."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV652909; AAT75279.1; -;
FT NON_TER 1 293
FT NON_TER 293 293
SQ SEQUENCE 293 AA; 32700 MW; C89B45D4DFCB7775 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
118 CHAVC 122

RESULT 15

Q692R2 ID Q692R2 PRELIMINARY; PRT; 293 AA.
AC Q692R2;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE P349 (Fragment).
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RA Herrera-Isidron L., Hernandez-Valencia M.C., Sanchez-Briseno V.,
RA Icurtiaga-Garciduenas D.R., Ochoa-Sanchez J.C., Rivera-Bustamante R.,
RA Martinez-Soriano J.P.;
RT "Molecular analysis of Citrus tristeza virus isolates from Mexico."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV652908; AAT75278.1; -;
FT NON_TER 1 293
FT NON_TER 293 293
SQ SEQUENCE 293 AA; 32172 MW; F587251FA4EC4156 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 293;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
118 CHAVC 122

RESULT 16

Q8T913 ID Q8T913 PRELIMINARY; PRT; 381 AA.
AC Q8T913; Q9VH34;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE AT07283p (CG12812-PA).
GN ORFNames=CG12812;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesen D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Baller J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabros B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gortell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosten D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskeirn D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang K., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Calniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [8]
DR EMBL; AY075174; AAL68044.1; -;
DR EMBL; AE003685; AAF54486.2; -;
DR IntAct; Q8T913; -;
DR FlyBase; FBgn0037781; CG12812.
SQ SEQUENCE 381 AA; 43725 MW; 012595FB8830BC9C CRC64;

Query Match 100.0%; Score 34; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 338 CHAVC 342

RESULT 17
Q7X8U8
ID Q7X8U8 PRELIMINARY; PRT; 382 AA.
AC Q7X8U8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNB0026E15.3 protein.
GN Name=OSJNB0026E15.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Wu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang W.,

RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL607008; CA503685.2; -;
DR Gramene; Q7X8U8; -;
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006527; F_box_assoc.1.
DR InterPro; IPR011043; Gal_oxid_central.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR TIGRFAMs; TIGR01640; F_box_assoc.1; 1.
DR PROSITE; PS0181; FBOX; 1.
SQ SEQUENCE 382 AA; 42864 MW; CF7B92144C7C8E2D CRC64;

Query Match 100.0%; Score 34; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 36 CHAVC 40

RESULT 18
Q769C8
ID Q769C8 PRELIMINARY; PRT; 400 AA.
AC Q769C8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cold-active esterase.
GN Name=Psy8at;
OS Psychrobacter sp. Ant300.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=235460;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ant300;
RA Kulakova L., Galkin A., Nakayama T., Nishino T., Esaki N.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB12812; BAD06009.1; -;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002168; Lipolytic enzyme.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000379; Ser_estra.
DR PROSITE; PS01173; LIPASE_GDXG_HIS; 1.
DR PROSITE; PS01142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 400 AA; 43683 MW; 108D59146AB86FDB CRC64;

Query Match 100.0%; Score 34; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 158 CHAVC 162

RESULT 19
Q9L514
ID Q9L514 PRELIMINARY; PRT; 400 AA.
AC Q9L514;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lipase.
GN Name=lip;
OS Psychrobacter sp. (strain St1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

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OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=125076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=St1;
RA Kulakova L., Galkin A., Kurihara T., Yoshimura T., Esaki N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260707; AAF70342.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002168; Lipolytic enzyme.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR003379; Ser esters.
DR PROSITE; PS01173; LIPASE_GDXG_HTS; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 400 AA; 4368 MW; 1D8D59146ABE6FDB CRC64;

Query Match 100.0%; Score 34; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 158 CHAVC 162

RESULT 20
Q9FRE7
ID Q9FRE7 PRELIMINARY; PRT; 424 AA.
AC Q9FRE7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OSUNBa0013M12.13.
GN Name=OSUNBa0013M12.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan O., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zisemann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC082644; AAG46124.1; -.
DR Gramene; Q9FRE7; -.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 424 AA; 46722 MW; 19B44C809CF41F02 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 39 CHAVC 43

RESULT 21
Q7QVC3
ID Q7QVC3 PRELIMINARY; PRT; 465 AA.
AC Q7QVC3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_542_47587_46190.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RL "Draft sequence of the Giardia lamblia genome.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC801000082; EAA39016.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR009030; Grow_Fac_recept.
DR PRINTS; PR00353; 4FE4SPRDOXIN.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 1.
SQ SEQUENCE 465 AA; 48977 MW; 83D00A8A5357D7DC CRC64;

Query Match 100.0%; Score 34; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 75 CHAVC 79

RESULT 22
Q9MZU5
ID Q9MZU5 PRELIMINARY; PRT; 537 AA.
AC Q9MZU5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Intercellular adhesion molecule-1 precursor.
GN Name=ICAM-1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=domestic breed; TISSUE=Aorta;
RA Stocker C., Sugars K., Yarwood H., Delikouras A., Dorling A.,
RA Lechler R., Landis C., Morley B., Haskard D.;
RT "Cloning of porcine ICAM-1 and characterization of ITS induction on
RT endothelial cells by cytokines.";
RL J. Immunol. 0:0-0(1999)
DR HSSP; AF156712; AAF80287.1; -.
DR HSSP; P05362; IIC1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003988; ICAM.
DR InterPro; IPR003987; ICAM_VCAM-1.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF03921; ICAM_N; 1.
DR PRINTS; PR01473; ICAM.
DR PRINTS; PR01472; ICAMVCAM1.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 537 intercellular adhesion molecule-1.

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SQ SEQUENCE 537 AA; 58430 MW; 47DA0F0F3C7C5CD54 CRC64;
Query Match 100.0%; Score 34; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 96 CHAVC 100

RESULT 23
Q69T84 PRELIMINARY; PRT; 544 AA.
AC Q69T84
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative P450.
GN Oryza sativa (japonica cultivar-group).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone: P0652D10."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL: AP004757; BAD33240.1;
DR GO: 0004497; P: monooxygenase activity; IEA.
DR GO: 0006118; P: electron transport; IEA.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR002401; EP450I.
DR Pfam: PF00067; P450; 1
DR PRINTS: PRO0463; EP450I.
DR PRINTS: PRO0385; P450.
DR PROSITE: PS00059; ADH_ZINC; UNKNOWN 1.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 544 AA; 61150 MW; 08F7A97974D0F5E1 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 221 CHAVC 225

RESULT 24
Q70Y47 PRELIMINARY; PRT; 660 AA.
AC Q70Y47
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_572_62459_60477.
OS Giardia lamblia ATCC 5803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AACB01000053; EAA40025.1;
DR GO: 0005489; P: electron transporter activity; IEA.
DR GO: 0005506; P: iron ion binding; IEA.
DR GO: 0006118; P: electron transport; IEA.
DR InterPro: IPR006058; 2Fe2S fd BS.
DR InterPro: IPR001450; 4Fe4S ferredoxin.
DR InterPro: IPR000345; CytC heme BS.
DR InterPro: IPR005127; Giardia VSP.
DR InterPro: IPR009030; Grow_fac_recept.
DR Pfam: PF03302; VSP; 1.
DR PRINTS: PRO0353; 4FE4SFRDOXIN.
DR PROSITE: PS00197; 2FE2S FERREDOXIN; UNKNOWN 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 660 AA; 66878 MW; 9AC79667499ED91B CRC64;

Query Match 100.0%; Score 34; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 282 CHAVC 286

RESULT 25
P87587 PRELIMINARY; PRT; 3107 AA.
AC P87587
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P346.
OS Citrus tristeza virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Closterovirus.
OX NCBI_TaxID=12162;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=vt;
RX MEDLINE=96406950; PubMed=8811037;
RA Mawassi M., Mietkiewska E., Gofman R., Yang G., Bar-Joseph M.;
RT "Unusual sequence relationships between two isolates of citrus
tristeza virus."
RL J. Gen. Virol. 77:2359-2364(1996).
DR EMBL: U56902; AAB38755.1;
DR GO: 0008174; P: RNA methyltransferase activity; IEA.
DR GO: 0003723; P: RNA binding; IEA.
DR GO: 0003724; P: RNA helicase activity; IEA.
DR GO: 0003968; P: RNA-directed RNA polymerase activity; IEA.
DR GO: 0006396; P: RNA processing; IEA.
DR GO: 0019079; P: viral genome replication; IEA.
DR InterPro: IPR008749; Peptidase C42.
DR InterPro: IPR000606; Viral_helicase1.
DR InterPro: IPR002588; V_methyltrans.
DR Pfam: PF05533; Peptidase C42; 2.
DR Pfam: PF01443; Viral_helicase1; 1.
DR Pfam: PF01660; Vmethyltransf; 1.
SQ SEQUENCE 3107 AA; 346659 MW; 02B748F693BE89CB CRC64;

Query Match 100.0%; Score 34; DB 2; Length 3107;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 594 CHAVC 598

RESULT 26
O10467

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ID O10467 PRELIMINARY; PRT; 3115 AA.
 AC O10467;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 347-kDa polyprotein.
 OS Citrus tristeza virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
 OC Closterovirus.
 OX NCBI_TaxID=12162;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SY568;
 RX MEDLINE=20007030; PubMed=10541017; DOI=10.1023/A:1008127224147;
 RA Yang Z.N., Mathews D.M., Dodds J.A., Mirkov T.E.;
 RT "Molecular characterization of an isolate of citrus tristeza virus
 RT that causes severe symptoms in sweet orange.";
 RL Virus Genes 19:131-142(1999).
 DR EMBL; AF001623; AAB57702.1; -;
 DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003724; F:RNA helicase activity; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006396; P:RNA processing; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.
 DR InterPro; IPR008749; Peptidase C42.
 DR InterPro; IPR000606; Viral helicase.
 DR InterPro; IPR002588; V_methyltrans.
 DR Pfam; PF05533; Peptidase C42; 2.
 DR Pfam; PF01443; Viral helicase1; 1.
 DR Pfam; PF01660; Vmethyltransf; 1.
 KW Polyprotein.
 SQ SEQUENCE 3115 AA; 347072 MW; B406EAFB38E73F9 CRC64;

 Query Match 100.0%; Score 34; DB 2; Length 3115;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CHAVC 5
 DB 600 CHAVC 604

 RESULT 27
 ID Q9IFX0 PRELIMINARY; PRT; 3115 AA.
 AC Q9IFX0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE P349 protein.
 OS Citrus tristeza virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
 OC Closterovirus.
 OX NCBI_TaxID=12162;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=730;
 RX MEDLINE=20347348; PubMed=10888625;
 RX DOI=10.1128/JVI.74.15.6856-6865.2000;
 RA Albiach-Marti M.R., Mawassi M., Gowda S., Satynaravana T., Hilf M.E.,
 RA Shanker S., Almira E.C., Vives M.C., Lopez C., Guerri J., Flores R.,
 RA Moreno P., Garnsey S.M., Dawson W.O.;
 RT "Sequences of citrus tristeza virus separated in time and space are
 RT essentially identical.";
 RL J. Virol. 74:6856-6865(2000).
 DR EMBL; AF260651; AAF70348.1; -;
 DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003724; F:RNA helicase activity; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006396; P:RNA processing; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.

DR InterPro; IPR008749; Peptidase C42.
 DR InterPro; IPR000606; Viral helicase1.
 DR InterPro; IPR002588; V_methyltrans.
 DR Pfam; PF05533; Peptidase C42; 2.
 DR Pfam; PF01443; Viral helicase1; 1.
 DR Pfam; PF01660; Vmethyltransf; 1.
 SQ SEQUENCE 3115 AA; 346874 MW; 6B97F494ED25AD63 CRC64;

 Query Match 100.0%; Score 34; DB 2; Length 3115;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CHAVC 5
 DB 600 CHAVC 604

 RESULT 28
 ID Q9WID7 PRELIMINARY; PRT; 3115 AA.
 AC Q9WID7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE P349 protein.
 OS Citrus tristeza virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
 OC Closterovirus.
 OX NCBI_TaxID=12162;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99190444; PubMed=10092023;
 RA Vives M.C., Rubio L., Lopez C., Navas-Castillo J., Albiach-Marti M.R.,
 RA Dawson W.O., Guerri J., Flores R., Moreno P.;
 RT "The complete genome sequence of the major component of a mild citrus
 RT tristeza virus isolate.";
 RL J. Gen. Virol. 80:811-816(1999).
 DR EMBL; Y18420; CAA77161.1; -;
 DR GO; GO:0008174; F:RNA methyltransferase activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003724; F:RNA helicase activity; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006396; P:RNA processing; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.
 DR InterPro; IPR008749; Peptidase C42.
 DR InterPro; IPR000606; Viral helicase1.
 DR InterPro; IPR002588; V_methyltrans.
 DR Pfam; PF05533; Peptidase C42; 2.
 DR Pfam; PF01443; Viral helicase1; 1.
 DR Pfam; PF01660; Vmethyltransf; 1.
 SQ SEQUENCE 3115 AA; 346982 MW; 3EEA613F605D5045 CRC64;

 Query Match 100.0%; Score 34; DB 2; Length 3115;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 CHAVC 5
 DB 600 CHAVC 604

 RESULT 29
 ID Q8BJT9 PRELIMINARY; PRT; 3122 AA.
 AC Q8BJT9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Polyprotein p349.
 OS Citrus tristeza virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
 OC Closterovirus.
 OX NCBI_TaxID=12162;


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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NEQ373
GN OrderedLocusNames=NEQ373;
OS Nanoarchaeum equitans.
OC Archaea; Nanoarchaeota; Nanoarchaeum.
OX NCBI_TaxID=160232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kin4-M;
RX MEDLINE=22946215; PubMed=14566062; DOI=10.1073/pnas.1735403100;
RA Waters E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M.,
RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,
RA Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,
RA Scell D., Stetter K.O., Short J.M., Noorderwier M.;
RT "The genome of Nanoarchaeum equitans: insights into early archaeal
RT evolution and derived parasitism.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988 (2003).
DR EMBL; AE017199; AAC39222.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR Pfam; PF00037; Fer4; 1.
DR PRINTS; PR00353; 4FE4SFRDOXN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
KW 4Fe-4S; Complete proteome; Iron; iron-sulfur; Metal-binding.
SQ SEQUENCE 75 AA; 7981 MW; B656508374A5CE9F9 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 75;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 17 CHAIC 21

RESULT 33
Q6AAV7 PRELIMINARY; PRT; 168 AA.
ID Q6AAV7
AC Q6AAV7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC
DE 4.6.1.12).
GN OrderedLocusNames=PPA0354;
OS Propionibacterium acnes.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacterineae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KPA171202 / DSM 16379;
RX PubMed=15286373; DOI=10.1126/science.1100330;
RA Brueggemann H., Henne A., Hostet F., Liesegang H., Wieser A.,
RA Strittmatter A., Hujer S., Duerre P., Gottschalk G.;
RT "The complete genome sequence of Propionibacterium acnes, a commensal
RT of human skin.";
RL Science 305:671-673 (2004).
DR EMBL; AE017283; AAT82109.1; -.
DR GO; GO:0008685; F:2-C-methyl-D-erythritol 2,4-cyclodiphosphat...; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0016114; P:terpenoid biosynthesis; IEA.
DR InterPro; IPR010925; MECPP synth.
DR InterPro; IPR003526; YgbB synth.
DR Pfam; PF02542; YgbB; 1.
DR PIRSF; PIRSF005911; MECPP synth; 1.
DR TIGRFAMS; TIGR00151; ispF; 1.
DR PROSITE; PS01350; ISP; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 168 AA; 16829 MW; DF6C56D1DD903042 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 113 CHAIC 117

RESULT 35
Q8Y2B0 PRELIMINARY; PRT; 273 AA.
ID Q8Y2B0
AC Q8Y2B0;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein RSC0426.
GN Name=RSC03995; OrderedLocusNames=RSC0426;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billaut A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguiet P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR EMBL; AL646059; CAD13954.1; -.
KW Complete proteome.
SQ SEQUENCE 273 AA; 28364 MW; 2B4AF9D2BA1BA14A CRC64;
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Thu Jul 28 07:51:38 2005

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Query Match          97.1%; Score 33; DB 2; Length 273;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      94 CHAIC 98

RESULT 36
O76856 PRELIMINARY; PRT; 383 AA.
AC O76856;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Precocathepsin D precursor (EC 3.4.23.5).
GN Name=ctsd;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Ax2, and Ax-2;
RX MEDLINE=99454799; PubMed=10523518;
RA Journet A.M., Chapel A., Jehan S., Adessi C., Freeze H., Klein G.,
RA Garin J.;
RT "Characterization of Dictyostelium discoideum cathepsin D. Molecular
RT cloning, gene disruption, endo-lysosomal localization and sugar
RT modifications."
RL J. Cell Sci. 112:3833-3843(1999).
CC -1- SIMILARITY: Belongs to peptidase family A1.
DR EMBL; Y16962; CAA76563.1; --
DR EMBL; AJ243946; CAB57223.1; --
DR HSSP; P00794; 4CMS.
DR DictyBase; DDB0215012; ctsd.
DR GO; GO:0004192; F:cathepsin D activity; IEA.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001461; Peptidase A1.
DR InterPro; IPR009007; Pept_Aspartic.
DR InterPro; IPR001969; Pept_Asp_AS.
DR PRINTS; PR00792; PEPsin.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Aspartyl protease; Hydrolase; Protease; Signal.
FT SIGNAL 18 Potential.
FT CHAIN 49 383 cathepsin D.
SQ SEQUENCE 383 AA; 41120 MW; CC8DE423AE1A280 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 383;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      263 CHAIC 267

RESULT 37
Q993M6 PRELIMINARY; PRT; 397 AA.
AC Q993M6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein 1 (Fragment).
GN Name=NS1;
OS Autonomus rat parvovirus RV-Y.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=155025;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=Yale;
RX MEDLINE=21102993; PubMed=11172095;
RA Ball-Goodrich L.J., Johnson E., Jacoby R.;
RT "Divergent replication kinetics of two phenotypically different
RT parvoviruses of rats.";
RL J. Gen. Virol. 82:537-546(2001).
DR EMBL; AF317513; AAK27438.1; --
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001257; Parvo NS1.
DR Pfam; PF01057; Parvo_NS1; 1.
KW Nonstructural protein.
FT NON_TER 1
SQ SEQUENCE 397 AA; 43959 MW; D62052E4767366BB CRC64;

Query Match          97.1%; Score 33; DB 2; Length 397;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      103 CHAIC 107

RESULT 38
VN34 ROTBS STANDARD; PRT; 402 AA.
ID VN34 ROTBS
AC P34717;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural RNA-binding protein 34 (NS34) (NCVp4).
GN Name=S6;
OS Bovine rotavirus (group C / strain Shintoku).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=33723;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93275758; PubMed=8389040;
RA Jiang B., Teunemiteu H., Gentsch J.R., Saif L.J., Glass R.I.;
RT "Nucleotide sequences of genes 6 and 10 of a bovine group C
RT rotavirus.";
RL Nucleic Acids Res. 21:2250-2250(1993).
CC -1- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
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CC -----
DR EMBL; L12390; --; NOT_ANNOTATED_CDS.
DR PIR; S35639; S35639.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR002873; Rota_NSP3.
DR Pfam; PF00035; darm; 1.
DR Pfam; PF01665; Rota_NSP3; 1.
DR SMART; SM00358; DSRM; 1.
DR PROSITE; PS00137; DS_RBD; 1.
KW Nonstructural protein; RNA-binding.
FT DOMAIN 384 400 DRBM.
SQ SEQUENCE 402 AA; 45081 MW; BBF553E9D955D49 CRC64;

Query Match          97.1%; Score 33; DB 1; Length 402;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
Db      280 CHAIC 284
```

```
RESULT 39
VN34_ROTFC STANDARD; PRT; 402 AA.
AC P27586;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural RNA-binding protein 34 (NS34) (NCVP4).
GN Name=S6;
OS Porcine rotavirus (group C / strain Cowden).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10916;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91361567; PubMed=1653496;
RA Qian Y.A., Jiang B.M., Saif L.J., Kang S.Y., Ojeh C.K., Green K.Y.;
RT "Molecular analysis of the gene 6 from a porcine group C rotavirus
  that encodes the NS34 equivalent of group A rotaviruses.";
RL Virology 184:752-757(1991).
CC -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M69115; AAA47087.1; -.
DR PIR; A41040; MXKRPC.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR002873; Rota_NSP3.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF01665; Rota_NSP3; 1.
DR PROSITE; PS50137; DS_RBD; 1.
KW Nonstructural protein; RNA-binding.
FT DOMAIN 384 400 DRBM.
SQ SEQUENCE 402 AA; 45125 MW; 8B11F7AC7FB5135C CRC64;

Query Match 97.1%; Score 33; DB 1; Length 402;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 280 CHAIC 284

RESULT 40
Q9PY95 PRELIMINARY; PRT; 402 AA.
AC Q9PY95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nonstructural protein 3.
GN Name=NSP3;
OS Human rotavirus (group C / strain Bristol).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus C.
OX NCBI_TaxID=31567;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol;
RX MEDLINE=20036633; PubMed=10567650;
RA James V.L.A., Lambden P.R., Deng Y., Caul E.O., Clarke I.N.;
RT "Molecular characterisation of human group C rotavirus genes 6, 7 and
  9.";
RL J. Gen. Virol. 80:3181-3187(1999).
DR EMBL; AJ132203; CAB52751.1; -.
DR HSSP; P03536; 1KNZ.
DR GO; GO:0005622; C:intracellular; IEA.
```

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DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR002873; Rota_NSP3.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF01665; Rota_NSP3; 1.
DR SMART; SM00358; DSRM; 1.
DR PROSITE; PS50137; DS_RBD; 1.
KW Nonstructural protein.
SQ SEQUENCE 402 AA; 45327 MW; D2E3D7F14B6E2E23 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 402;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 280 CHAIC 284

RESULT 41
Q9MIQ8 PRELIMINARY; PRT; 428 AA.
AC Q9MIQ8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein T17J13.120.
GN Name=T17J13.120;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138651; CAB71876.1; -.
DR PIR; T48008; T48008.
DR InterPro; IPR003480; Transferase.
DR Pfam; PF02458; Transferase; 1.
KW Hypothetical protein.
SQ SEQUENCE 428 AA; 47553 MW; 66C5155A161B26CA CRC64;

Query Match 97.1%; Score 33; DB 2; Length 428;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 153 CHAIC 157

RESULT 42
Q71159 PRELIMINARY; PRT; 665 AA.
AC Q71159;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein (Fragment).
GN Name=NS1;
OS Kilham rat virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=12441;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=U-Mass;
RX MEDLINE=98184569; PubMed=9525656;
RA Ball-Goodrich L.J., Leland S.E., Johnson E.A., Paturzo F.X.,
RA Jacoby R.O.;
RT "Rat parvovirus type 1: the prototype for a new rodent parvovirus
RT serogroup.";
RL J. Virol. 72:3289-3299(1998).
DR EMBL: AF036711; AAC40695.1; -.
DR GO: GO:0019012; C:virion; IEA.
DR GO: GO:0019079; P: viral genome replication; IEA.
DR InterPro: IPR001257; Parvo_NSI.
DR Pfam: PF01057; Parvo_NSI; I.
KW Nonstructural protein.
FT NON TER 1
SQ SEQUENCE 665 AA; 75375 MW; 778E29043417E409 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 665;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 371 CHAIC 375

RESULT 43
VNC5_PAVL3 STANDARD; PRT; 668 AA.
AC P36311;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Noncapsid protein NS-1 (Nonstructural protein NS1).
GN Name=NS1;
OS Parvovirus LuIII.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OC NCBI_TaxID=35339;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=93297126; PubMed=8517025;
RA Diffoot N., Chen K.C., Bates R.C., Lederma M.;
RT "The complete nucleotide sequence of parvovirus LuIII and localization
RT of a unique sequence possibly responsible for its encapsidation
RT pattern.";
RL Virology 192:339-345(1993).
CC -1- FUNCTION: Seems necessary for viral DNA replication.
CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
CC -----
DR EMBL: M81888; -. NOT_ANNOTATED_CDS.
DR PIR: A44276; A44276.
DR InterPro: IPR001257; Parvo_NSI.
DR Pfam: PF01057; Parvo_NSI; I.
DR KW ATP-binding; DNA replication; Noncapsid protein;
KW Nonstructural protein.
FT NP_BIND 399 406 ATP (Potential).
SQ SEQUENCE 668 AA; 75846 MW; CA669049F8F86B53 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 668;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 378 CHAIC 382

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RESULT 44

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VNC5_MUMIV STANDARD; PRT; 672 AA.
ID VNC5_MUMIV STANDARD; PRT; 672 AA.
AC P07300; P10837;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).
GN Name=NS1;
OS Murine minute virus (strain MVMi) (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OC NCBI_TaxID=10795;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice,
RT MVM(1), and comparison with the DNA sequence of the fibrotropic
RT prototype strain.";
RL J. Virol. 57:656-669(1986).
RN [2];
RP SEQUENCE FROM N.A.
RX MEDLINE=85242059; PubMed=3855242;
RA Sahli R., McMaster G.K., Hirt B.;
RT "DNA sequence comparison between two tissue-specific variants of the
RT autonomous parvovirus, minute virus of mice.";
RL Nucleic Acids Res. 13:3617-3633(1985).
CC -1- FUNCTION: Seems necessary for viral DNA replication.
CC -1- SUBUNIT: Forms homooligomers. Interacts with human SYNCRIP (By
CC similarity).
CC -1- DOMAIN: The N-terminus (residues 1-275) possess a negative effect
CC on transactivation (By similarity).
CC -1- DOMAIN: The C-terminus (residues 543-672) possess an activation
CC domain (By similarity).
CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
CC -----
DR EMBL: X02481; -. NOT_ANNOTATED_CDS.
DR EMBL: M12032; AAA69567.1; -.
DR InterPro: IPR001257; Parvo_NSI; I.
DR Pfam: PF01057; Parvo_NSI; I.
DR KW ATP-binding; DNA replication; Noncapsid protein;
KW Nonstructural protein.
FT DOMAIN 1 276 Interacts with SYNCRIP (By similarity).
FT NP_BIND 399 406 ATP (Potential).
FT CONFLICT 597 597 I -> L (in Ref. 2).
SQ SEQUENCE 672 AA; 76140 MW; 25F025FE328B4DF0 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 378 CHAIC 382

RESULT 45
VNC5_MUMIV STANDARD; PRT; 672 AA.
ID VNC5_MUMIV STANDARD; PRT; 672 AA.
AC P03134;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVPI).

```

GN Name=NS1;
 OS Murine minute virus (Murine parvovirus).
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxId=10794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83143341; PubMed=6298737;
 RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
 RT "The complete DNA sequence of minute virus of mice, an autonomous
 RT parvovirus.";
 RL Nucleic Acids Res. 11:999-1018(1983).
 RN [2]
 RP HOMOLOGIZATION, AND INTERACTION WITH SYNCRIP.
 RX MEDLINE=99102562; PubMed=9847309;
 RA Harris C.E., Boden R.A., Astell C.R.;
 RT "A novel heterogeneous nuclear ribonucleoprotein-like protein
 RT interacts with NS1 of the minute virus of mice.";
 RL J. Virol. 73:72-80(1999).
 CC -1- FUNCTION: Seems necessary for viral DNA replication.
 CC -1- SUBUNIT: Forms homooligomers. Interacts with human SYNCRIP.
 CC -1- DOMAIN: The N-terminus (residues 1-275) possess a negative effect
 CC on transactivation.
 CC -1- DOMAIN: The C-terminus (residues 543-672) possesses an activation
 CC domain.
 CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
 CC -----
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 CC -----
 DR EMBL; J02275; AAA67109.1; -;
 DR EMBL; V01115; CAA24309.1; ALT_INIT.
 DR PIR; A03696; UYPVIM.
 DR TRANSFAC; T02375; -;
 DR InterPro; IPR001257; Parvo NS1.
 DR Pfam; PF01057; Parvo NS1; I.
 KW ATP-binding; DNA replication; Noncapsid protein;
 KW Nonstructural protein.
 FT DOMAIN 1 276 ATP (Potential).
 FT NP BIND 399 406
 SQ SEQUENCE 672 AA; 76248 MW; 50298F27662E3C1D CRC64;
 Query Match 97.1%; Score 33; DB 1; Length 672;
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 378 CHAIC 382
 RESULT 46
 VNCS_PAVHH STANDARD; PRT; 672 AA.
 AC P03133;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Noncapsid protein NS-1 (Nonstructural protein NS1) (NCVP1).
 GN Name=NS1;
 OS Hamster parvovirus H1.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxId=10799;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83112183; PubMed=6823009;
 RA Rhode S.L. III, Paradiso P.R.;
 RT "Parvovirus genome: nucleotide sequence of H-1 and mapping of its
 RT genes by hybrid-arrested translation.";

RL J. Virol. 45:173-184(1983).
 CC -1- FUNCTION: Seems necessary for viral DNA replication.
 CC -1- SIMILARITY: Belongs to the parvoviruses noncapsid protein family.
 CC -----
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 CC -----
 DR EMBL; X01457; CAA25689.1; -;
 DR PIR; A03695; UYPVV1.
 DR InterPro; IPR001257; Parvo NS1.
 DR Pfam; PF01057; Parvo NS1; I.
 KW ATP-binding; DNA replication; Noncapsid protein;
 KW Nonstructural protein.
 FT NP BIND 399 406 ATP (Potential).
 SQ SEQUENCE 672 AA; 75993 MW; 12F331142F72AA6D CRC64;
 Query Match 97.1%; Score 33; DB 1; Length 672;
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 378 CHAIC 382
 RESULT 47
 P88899 PRELIMINARY; PRT; 672 AA.
 ID P88899
 AC P88899;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Non-capsid protein.
 GN Name=NS1;
 OS Kilham rat virus.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxId=12441;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brown D.W., Like A.A.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79033; AAB38326.1; -;
 DR GO; GO:0019079; P:Viral genome replication; IEA.
 DR InterPro; IPR001257; Parvo NS1.
 DR Pfam; PF01057; Parvo NS1; I.
 SQ SEQUENCE 672 AA; 76056 MW; 0299B36871A0A10A CRC64;
 Query Match 97.1%; Score 33; DB 2; Length 672;
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 378 CHAIC 382
 RESULT 48
 Q8JV14 PRELIMINARY; PRT; 672 AA.
 ID Q8JV14
 AC Q8JV14;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nonstructural protein 1.
 GN Name=NS1;
 OS Rat minute virus 1c.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxId=172387;

```

RN  SEQUENCE FROM N.A.
RX  MEDLINE=22120170; PubMed=12124471;
RA  Wan C.-H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RT  "Molecular characterization of three newly recognized rat
RL  parvoviruses.";
RN  J. Gen. Virol. 83:2075-2083 (2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Pintel D.J., Soderlund-Venermo M., Riley L.K.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332884; AAM93279.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo NS1.
DR  Pfam; PF01057; Parvo NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 75988 MW; 52DF6549349CF3FD CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

RESULT 49
Q8JV16
ID  Q8JV16      PRELIMINARY;      PRT;      672 AA.
AC  Q8JV16;
DT  01-OCT-2002 (TReMBLrel. 22, Created)
DT  01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT  01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE  Nonstructural protein 1.
GN  Name=NS1;
OS  Rat minute virus 1b.
OC  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX  NCBI_TaxID=172386;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22120170; PubMed=12124471;
RA  Wan C.-H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RT  "Molecular characterization of three newly recognized rat
RL  parvoviruses.";
RN  J. Gen. Virol. 83:2075-2083 (2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Pintel D.J., Soderlund-Venermo M., Riley L.K.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332883; AAM93277.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo NS1.
DR  Pfam; PF01057; Parvo NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 76201 MW; C2F1A71F6EF449A6 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

RESULT 50
Q8JV18
ID  Q8JV18      PRELIMINARY;      PRT;      672 AA.
AC  Q8JV18;
DT  01-OCT-2002 (TReMBLrel. 22, Created)

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DT  01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT  01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE  Nonstructural protein 1.
GN  Name=NS1;
OS  Rat minute virus 1a.
OC  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX  NCBI_TaxID=172385;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22120170; PubMed=12124471;
RA  Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RT  "Molecular characterization of three newly recognized rat
RL  parvoviruses.";
RN  J. Gen. Virol. 83:2075-2083 (2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Pintel D.J., Soderlund-Venermo M., Riley L.K.;
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332882; AAM93275.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo NS1.
DR  Pfam; PF01057; Parvo NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 76059 MW; 63D8B9BFP99E07B3 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

RESULT 51
Q8JV28
ID  Q8JV28      PRELIMINARY;      PRT;      672 AA.
AC  Q8JV28;
DT  01-OCT-2002 (TReMBLrel. 22, Created)
DT  01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT  01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE  Nonstructural protein 1.
GN  Name=ns1;
OS  Kilham rat virus.
OC  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX  NCBI_TaxID=12441;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22120170; PubMed=12124471;
RA  Wan C.H., Soderlund-Venermo M., Pintel D.J., Riley L.K.;
RT  "Molecular characterization of three newly recognized rat
RL  parvoviruses.";
RN  J. Gen. Virol. 83:2075-2083 (2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Wan C.-H., Soderlund-Venermo M., Pintel D., Riley L.K.;
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF321230; AAM93272.1; -.
DR  GO; GO:0019012; C:virion; IEA.
DR  GO; GO:0019079; P:viral genome replication; IEA.
DR  InterPro; IPR001257; Parvo NS1.
DR  Pfam; PF01057; Parvo NS1; I.
KW  Nonstructural protein.
SQ  SEQUENCE 672 AA; 75987 MW; 22B4611C20CDB6E9 CRC64;

Query Match          97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CHAVC 5
Db  378 CHAIC 382

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RESULT 52

Q83429 Q83429 PRELIMINARY; PRT; 672 AA.
AC Q83429;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein 1.
GN Name=NS1;
OS Mouse parvovirus 1.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=35340;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94365951; PubMed=8083985;
RA Ball-Goodrich L.J., Johnson E.;
RT "Molecular characterization of a newly recognized mouse parvovirus.";
RL J. Virol. 68:6476-6486(1994).
DR EMBL; U12469; AAA61405.1; -;
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001257; Parvo NS1.
DR Pfam; PF01057; Parvo NS1; I.
KW Nonstructural protein.
SQ SEQUENCE 672 AA; 76112 MW; 31C6365276727363 CRC64;

Query Match 97.1%; Score 33; DB 2; Length 672;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|

Db 378 CHAIC 382

RESULT 53

Q84363 Q84363 PRELIMINARY; PRT; 721 AA.
AC Q84363;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein.
GN Name=NS1;
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic prototype strain".
RT J. Virol. 57:656-669(1986).
DR EMBL; M12032; AAA69566.1; -;
DR PIR; A23008; UYFVIN.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001257; Parvo NS1.
DR Pfam; PF01057; Parvo NS1; I.
KW Nonstructural protein.
SQ SEQUENCE 721 AA; 81862 MW; 9FD29C327C7F4BBF CRC64;

Query Match 97.1%; Score 33; DB 2; Length 721;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|

Db 427 CHAIC 431

RESULT 54

Q84365 Q84365 PRELIMINARY; PRT; 721 AA.
AC Q84365;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein.
GN Name=NS1;
OS Murine minute virus (Murine parvovirus).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10794;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MVM;
RX MEDLINE=83143341; PubMed=6298737;
RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
RT "The complete DNA sequence of minute virus of mice, an autonomous parvovirus.";
RT Nucleic Acids Res. 11:999-1018(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MVM;
RX MEDLINE=86115415; PubMed=3502703;
RA Astell C.R., Gardiner E.M., Tattersall P.;
RT "DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic prototype strain".
RT J. Virol. 57:656-669(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=MVM;
RX MEDLINE=87061199; PubMed=3783817;
RA Morgan W.R., Ward D.C.;
RT "Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAs".
RT J. Virol. 60:1170-1174(1986).
DR EMBL; J02275; AAA67108.1; -;
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001257; Parvo NS1.
DR Pfam; PF01057; Parvo NS1; I.
KW Nonstructural protein.
SQ SEQUENCE 721 AA; 81896 MW; 18391758E42F0DCF CRC64;

Query Match 97.1%; Score 33; DB 2; Length 721;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|

Db 427 CHAIC 431

RESULT 55

Q6ES22 Q6ES22 PRELIMINARY; PRT; 815 AA.
AC Q6ES22;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative far-red impaired response protein.
GN Name=P0472P10.13-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;

Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AP004877; BAD28228.1; -;
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR004330; PAR1.
 DR InterPro; IPR003657; WRKY.
 DR InterPro; IPR006564; Znf_PMZ.
 DR InterPro; IPR007527; Znf_SWIM.
 DR Pfam; PF03101; PAR1; 1.
 DR Pfam; PF04434; SWIM; 1.
 DR SMART; SM00575; Znf_PMZ; 1.
 DR PROSITE; PS0811; WRKY; 1.
 SQ SEQUENCE 815 AA; 92895 MW; 003FD2ED7784E1C4 CRC64;
 Query Match 97.1%; Score 33; DB 2; Length 815;
 Best Local Similarity 80.0%; Pred. No. 6.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 352 CHAIC 356
 RESULT 56
 Q7XDU9 PRELIMINARY; PRT; 929 AA.
 AC Q7XDU9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative mutator protein.
 GN ORFNames=OSJNBa0068N06.23;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 SEQUENCE FROM N.A.
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017100; AAP54042.1; -;
 DR Gramene; Q7XDU9; -;
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR SMART; SM00343; Znf_C2HC; 1.
 SQ SEQUENCE 929 AA; 104564 MW; FE8FAD5D49F09300 CRC64;
 Query Match 97.1%; Score 33; DB 2; Length 929;
 Best Local Similarity 80.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 719 CHAIC 723
 RESULT 57
 Q6L4D3 PRELIMINARY; PRT; 1092 AA.
 AC Q6L4D3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSJNBa0088M05.7;
 GN Name=OSJNBa0088M05.7;
 OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 SEQUENCE FROM N.A.
 RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Heu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Lu H.-P., Shaw J.-F.;
 RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC136222; AAT38055.1; -;
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR InterPro; IPR006564; Znf_PMZ.
 DR InterPro; IPR007527; Znf_SWIM.
 DR Pfam; PF04434; SWIM; 1.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR SMART; SM00575; Znf_PMZ; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1092 AA; 122243 MW; 8A9B50FD758C0EA5 CRC64;
 Query Match 97.1%; Score 33; DB 2; Length 1092;
 Best Local Similarity 80.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 805 CHAIC 809
 RESULT 58
 SCX1_MESTA STANDARD; PRT; 64 AA.
 ID SCX1_MESTA
 AC P60277;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Neurotoxin.
 OS Mesobuthus tamulus (Eastern Indian scorpion) (Buthus tamulus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthida; Buthoidea; Buthidae; Mesobuthus.
 OX NCBI_TaxID=34647;
 RN [1]
 SEQUENCE FROM N.A.
 RA Sharma M., Yadav S., Karthikeyan S., Kumar S., Paramasivam M.,
 RA Srinivasan A., Singh T.P.;
 RA "Three-dimensional structure of a neurotoxin from red scorpion (Buthus tamulus) at 2.2-A resolution."
 RT Submitted (AUG-2000) to the PDB data bank.
 CC -1- FUNCTION: Inhibits sodium channels (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
 DR PDB; IDQ7; X-ray; -;
 DR InterPro; IPR002061; Scorpion_toxinL.
 DR PRINTS; PR00285; SCORPNTOXIN.
 DR ProDom; PD000908; Scorpion_toxinL; 1.
 KW 3D-structure; Ionic channel inhibitor; Neurotoxin;
 KW Sodium channel inhibitor; Toxin.
 FT DISULFID 12 63
 FT DISULFID 16 36
 FT DISULFID 22 46
 FT DISULFID 26 48
 SQ SEQUENCE 64 AA; 7041 MW; 06A852E2F5B0B934 CRC64;
 Query Match 91.2%; Score 31; DB 1; Length 64;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5

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Db          |||:|
           22 CHALC 26

RESULT 59
Q8D488      PRELIMINARY;      PRT; 108 AA.
AC Q8D488;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=VW21423;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
  Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016813; AAO08302.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 108 AA; 11846 MW; FB92F8EA3E170EAA CRC64;

Query Match          91.2%; Score 31; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   ||:|
Db 57 CHSVC 61

RESULT 60
Q7MFR2      PRELIMINARY;      PRT; 116 AA.
AC Q7MFR2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein VWA0258.
GN OrderedLocusNames=VWA0258;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
  Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
  Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
  pathogen."
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005345; BAC96284.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 116 AA; 12693 MW; 19B1D5E12C9C108B CRC64;

Query Match          91.2%; Score 31; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   ||:|
Db 65 CHSVC 69

RESULT 61
Q8C3T4      PRELIMINARY;      PRT; 118 AA.
AC Q8C3T4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
  library, clone:D430021L16 product:hypothetical protein, full insert
  sequence.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 403:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
  Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaki S., Inoue K., Izawa M., Ohara E., Watahiki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
  Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
  Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
  Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
  Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
  Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
  Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
  Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL

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DR EMBL; AK04985; BAC39329.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 118 AA; 12409 MW; 9DE6A7E88C8575BC CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 118;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 Db 114 CHALC 118
 RESULT 62
 Q8QY23
 ID Q8QY23 PRELIMINARY; PRT; 124 AA.
 AC Q8QY23;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thymidylate synthase-like protein.
 OS Rana tigrina ranavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.
 OX NCBI_TaxID=160691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21874850; PubMed=11878922; DOI=10.1006/viro.2001.1245;
 RA He J.G., Lu L., Deng M., He H.H., Weng S.P., Wang X.H., Zhou S.Y.,
 RA Long Q.X., Wang X.Z., Chan S.M.;
 RA "Sequence analysis of the complete genome of an iridovirus isolated
 RT from the tiger frog."
 RL Virology 292:185-197(2002).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC -1- dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 CC EMBL; AF389451; AAL77812.1; -;
 DR HSSP; P45352; 1RTS.
 DR GO; GO:0008168; P:methyltransferase activity; IEA.
 DR GO; GO:0004799; P:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt_1.
 DR PRINTS; PR00108; THYMSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR MethyItransferase; Nucleotide biosynthesis; Transferase.
 KW SEQUENCE 124 AA; 14002 MW; 7123A290B15E6D21 CRC64;
 SQ SEQUENCE 124 AA; 14002 MW; 7123A290B15E6D21 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 124;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 Db 6 CHAMC 10
 RESULT 63
 Q8TWX8
 ID Q8TWX8 PRELIMINARY; PRT; 139 AA.
 AC Q8TWX8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ferredoxin.
 GN OrderedLocusNames=MK0903;
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
 RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
 RA Shcherebina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Nacale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 RT and monophyly of archaeal methanogens."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 DR EMBL; AE010380; AAM02116.1; -;
 DR HSSP; P00193; 1DUR.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR Pfam; PF00037; Fer4; 2.
 DR PRINTS; PR00353; 4FE4SPRDOXIN
 DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
 KW 4FE-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
 SQ SEQUENCE 139 AA; 15190 MW; CE929F07722287FE CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 139;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 Db 91 CHSVC 95
 RESULT 64
 Q91019
 ID Q91019 PRELIMINARY; PRT; 168 AA.
 AC Q91019;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE TRL10.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=11pan, Davis, and 33spa;
 RX MEDLINE=21635521; PubMed=11773418;
 RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
 RT "Identification of glycoprotein gpTRL10 as a structural component of
 RT human cytomegalovirus."
 RL J. Virol. 76:1450-1460(2002).
 DR EMBL; AF432091; AAL27473.1; -;
 DR EMBL; AF432084; AAL27466.1; -;
 DR EMBL; AF432087; AAL27469.1; -;
 DR Pfam; PF06084; Cytomega TRL10; 1.
 SQ SEQUENCE 168 AA; 18762 MW; B18FA2748C12F431 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 168;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 Db 57 CHAMC 61
 RESULT 65
 Q6SX91
 ID Q6SX91 PRELIMINARY; PRT; 168 AA.
 AC Q6SX91;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE RL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6397;
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
RA Davison A.J.;
RT "Genetic content of wild-type human cytomegalovirus.";
RL J. Gen. Virol. 85:1301-1312(2004).
DR EMBL; AY446861; AAR31252.1; -.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 168 AA; 18776 MW; B18FA2748C144281 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 168;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 57 CHAMC 61

RESULT 66
Q6SXA8 PRELIMINARY; PRT; 168 AA.
ID Q6SXA8
AC Q6SXA8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Toledo;
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
RA Davison A.J.;
RT "Genetic content of wild-type human cytomegalovirus.";
RL J. Gen. Virol. 85:1301-1312(2004).
DR EMBL; AY446860; AAR31235.1; -.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 168 AA; 18763 MW; CODA9297670DAD86 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 168;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 57 CHAMC 61

RESULT 67
Q914P6 PRELIMINARY; PRT; 170 AA.
ID Q914P6
AC Q914P6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TRL10.

OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22alt;
RX MEDLINE=21635521; PubMed=11773418;
RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
RT "Identification of glycoprotein gpRL10 as a structural component of
human cytomegalovirus.";
RL J. Virol. 76:1450-1460(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Merlin;
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
RA Davison A.J.;
RT "Genetic content of wild-type human cytomegalovirus.";
RL J. Gen. Virol. 85:1301-1312(2004).
DR EMBL; AY446894; AAR31564.1; -.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 170 AA; 18974 MW; 7C850AB8EF36E61C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 170;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 59 CHAMC 63

RESULT 68
Q914P8 PRELIMINARY; PRT; 170 AA.
ID Q914P8
AC Q914P8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TRL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7ro;
RX MEDLINE=21635521; PubMed=11773418;
RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
RT "Identification of glycoprotein gpTRL10 as a structural component of
human cytomegalovirus.";
RL J. Virol. 76:1450-1460(2002).
DR EMBL; AF432085; AAL27467.1; -.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 170 AA; 19031 MW; 7B7827917BFCB80C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 170;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 59 CHAMC 63

RESULT 69
Q914P9 PRELIMINARY; PRT; 170 AA.
ID Q914P9
AC Q914P9

01-DEC-2001 (TrEMBLrel. 19, Created)
 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 TRL10.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=7330et;
 RX MEDLINE=21635521; PubMed=11773418;
 RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
 RT "Identification of glycoprotein gpTRL10 as a structural component of
 human cytomegalovirus.";
 RL J. Virol. 76:1450-1460(2002).
 DR EMBL; AF432083; AAL27465.1; -;
 DR Pfam; PF06084; Cytomega_TRL10; 1.
 SQ SEQUENCE 170 AA; 19032 MW; 7876C7917BFCB80C CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 170;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 59 CHAMC 63
 RESULT 70
 ID IR10 HCMVA STANDARD; PRT; 171 AA.
 AC P16808;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Hypothetical protein IRL10 precursor (TRL10).
 OS Human cytomegalovirus (strain AD169).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90269039; PubMed=2161319;
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
 RA Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
 RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 RT "Analysis of the protein-coding content of the sequence of human
 cytomegalovirus strain AD169.";
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 CC -----
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 CC -----
 CC EMBL; X17403; CRA35300.1; -;
 DR PIR; S09903; S09903.
 DR InterPro; IPR009284; Cytomega_TRL10.
 DR Pfam; PF06084; Cytomega_TRL10-1.
 KW Glycoprotein; Hypothetical protein; Signal; Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 171 Hypothetical protein IRL10.
 FT TRANSMEM 80 100 Potential.
 FT CARBOHYD 48 48 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 171 AA; 19034 MW; 2C2E8AD869419B86 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 171;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 60 CHAMC 64
 RESULT 71
 ID Q914P7 PRELIMINARY; PRT; 171 AA.
 AC Q914P7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE TRL10.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5929C;
 RX MEDLINE=21635521; PubMed=11773418;
 RA Spaderna S., Blessing H., Bogner E., Britt W., Mach M.;
 RT "Identification of glycoprotein gpTRL10 as a structural component of
 human cytomegalovirus.";
 RL J. Virol. 76:1450-1460(2002).
 DR EMBL; AF432088; AAL27470.1; -;
 DR Pfam; PF06084; Cytomega_TRL10; 1.
 SQ SEQUENCE 171 AA; 19035 MW; 2C206AD869419B86 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 171;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 60 CHAMC 64
 RESULT 72
 ID Q69029 PRELIMINARY; PRT; 171 AA.
 AC Q69029; Q7M5U1;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE HCMVTRL10 = IRL10 protein.
 GN Name=HCMVTRL10 = IRL10;
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AD169;
 RX MEDLINE=90269039; PubMed=2161319;
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
 RA Horsnell T., Hutchison III C.A., Kouzarides T., Martignetti J.A.,
 RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 RT "Analysis of the protein coding content of human cytomegalovirus
 strain AD169.";
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AD169;
 RX MEDLINE=92199238; PubMed=1666311;
 RA Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Chee M.S.,
 RA Hutchison III C.A., Kouzarides T., Martignetti J.A., Preddie E.,
 RA Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 RT "The DNA sequence of the human cytomegalovirus genome.";

RL DNA Seq. 2:1-12(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AD169;
RA Chee M.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=AD169;
RX MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;
RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,
RA Alcendor D.J., McGeoch D.J., Hayward G.S.;
RT "The human cytomegalovirus genome revisited: comparison with the
RT chimpanzee cytomegalovirus genome.";
RL J. Gen. Virol. 84:17-28(2003).
DR EMBL; X17403; CAA35458.1; -.
DR EMBL; BK000394; DAA00091.1; -.
DR PIR; S09759; S09759.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 171 AA; 19035 MW; AE2E8AD0CB47D988 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 60 CHAMC 64

RESULT 73

Q6SX75 Q6SX75 PRELIMINARY; PRT; 171 AA.
AC Q6SX75;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE RL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3301;
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
RA Davison A.J.;
RT "Genetic content of wild-type human cytomegalovirus.";
RL J. Gen. Virol. 85:1301-1312(2004).
DR EMBL; AY446862; AAR31268.1; -.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 171 AA; 19016 MW; 23F9220850767E96 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 60 CHAMC 64

RESULT 74

Q6SXC6 Q6SXC6 PRELIMINARY; PRT; 171 AA.
AC Q6SXC6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE RL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3;
RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.,
RA Davison A.J.;
RT "Genetic content of wild-type human cytomegalovirus.";
RL J. Gen. Virol. 85:1301-1312(2004).
DR EMBL; AY446859; AAR31217.1; -.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 171 AA; 19006 MW; CDA4427AE376BE25 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 60 CHAMC 64

RESULT 75

Q7M6G1 Q7M6G1 PRELIMINARY; PRT; 171 AA.
AC Q7M6G1;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE RL10.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD169;
RX MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;
RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,
RA Alcendor D.J., McGeoch D.J., Hayward G.S.;
RT "The human cytomegalovirus genome revisited: comparison with the
RT chimpanzee cytomegalovirus genome.";
RL J. Gen. Virol. 84:17-28(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK000394; DAA00228.1; -.
DR InterPro; IPR009284; Cytomega_TRL10.
DR Pfam; PF06084; Cytomega_TRL10; 1.
SQ SEQUENCE 171 AA; 19034 MW; 2C2E8AD869419B86 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 171;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 60 CHAMC 64

RESULT 76

Q8C2H6 Q8C2H6 PRELIMINARY; PRT; 222 AA.
AC Q8C2H6;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)


```

RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kunito H., Akiyama J., Nishi K., Kitsuunai T., Taghito H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Nishihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saiboh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akshira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
CC EMBL; AK088134; BAC40165.1; -.
DR HSSP; P45352; 1RTS.
DR MGD; MGI:98878; Tyms.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synt.; 1.
DR PRINTS; PR00108; THYMSNTHASE.
DR PRODOM; PD001180; Thymidylat synth.; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
FT NON TER
FT 1
SQ SEQUENCE 222 AA; 25209 MW; 3E8BDAF742DCC01 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 222;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 104 CHALC 108
|||:|
|||:|

RESULT 78
Q8WYK4 PRELIMINARY; PRT; 230 AA.
AC Q8WYK4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thymidylate synthase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592598; PubMed=12706868; DOI=10.1016/S0304-3835(03)00005-3;

SEQUENCE FROM N.A.
RA Hisatomi H., Tanemura H., Iizuka T., Katsumata K., Nagao K.,
RA Sumida H., Udagawa H., Hikiji K.;
RT "Differential alternative splicing expressions of thymidylate synthase
isoforms.";
RL Cancer Lett. 193:127-131(2003).
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
CC EMBL; AB077207; BAB83676.1; -.
DR HSSP; P04818; 1HYV.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR Pfam; PF00303; Thymidylat synt.; 1.
DR PRINTS; PR00108; THYMSNTHASE.
DR PRODOM; PD001180; Thymidylat synth.; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 230 AA; 26140 MW; D09F8316A504A02A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 230;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 112 CHALC 116
|||:|
|||:|

RESULT 79
Q8QNP2 PRELIMINARY; PRT; 232 AA.
AC Q8QNP2
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Esv-1-19.
GN Name=ORF 19;
OS Ectocarpus siliculosus virus.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
OX NCBI_TaxID=37665;
RN [1]_TaxID=37665;
RP SEQUENCE FROM N.A.
RC STRAIN=Esv-1;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF204951; AAK14445.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001841; Znf_king.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 232 AA; 26241 MW; 893749786BBB4D3 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 232;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 128 CHAMC 132
|||:|
|||:|

RESULT 80
Q9FYL9 PRELIMINARY; PRT; 251 AA.
AC Q9FYL9

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE F21J9.10 (Hypothetical protein Atlg24440).
 GN Name=Atlg24440;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.R.;
 RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.B.;
 RA "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M.,
 RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
 RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC000103; AAF97956.1; -;
 DR EMBL; AY085533; AAM62757.1; -;
 DR EMBL; BT000927; AANA1327.1; -;
 DR PIR; E86378; E86378.
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; E:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; F:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_ring.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 251 AA; 29487 MW; FCAA26695D467218 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 251;
 Best Local Similarity 80.0%; Pred. No. 5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 171 CHAMC 175

RESULT 81

Q7MU57 PRELIMINARY; PRT; 261 AA.
 AC Q7MU57;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MazG family protein.
 GN OrderedLocusNames=PGL1703;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=8337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=W83; PubMed=12949112;
 RX MEDLINE=22829867; PubMed=12949112;
 RX DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RA "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83.";
 RL J. Bacteriol. 185:5591-5601(2003).
 DR EMBL; AE017177; AAQ66714.1; -;
 DR TIGR; PGI703; -;
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR004518; MazG.
 DR InterPro; IPR011551; MazG_bact.
 DR Pfam; PF03819; MazG; 2.
 DR TIGRFAMs; TIGR00444; mazG; 1.
 KW Complete proteome.
 SQ SEQUENCE 261 AA; 29868 MW; E4720FD02BFF0ABC CRC64;

Query Match 91.2%; Score 31; DB 2; Length 261;

Best Local Similarity 80.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 82

Q9VDN1 PRELIMINARY; PRT; 272 AA.
 AC Q9VDN1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG4342-PA.
 GN ORFNames=CG4342;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Perryman S.M., Rossana C., Deng T., Vanin E.F., Johnson L.F.;
 RT "Sequence of a cDNA for mouse thymidylate synthase reveals striking
 RL similarity with the prokaryotic enzyme.";
 RN Mol. Biol. Evol. 3:313-321(1986).
 RP [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87057259; PubMed=3782103;
 RA Deng T., Li D., Jenh C.-H., Johnson L.F.;
 RT "Structure of the gene for mouse thymidylate synthase. Locations of
 RT introns and multiple transcriptional start sites.";
 RL J. Biol. Chem. 261:16000-16005(1986).
 RP [3]
 RP SEQUENCE OF 236-265 FROM N.A.
 RX MEDLINE=89128436; PubMed=2915925;
 RA Deng T., Li Y., Johnson L.F.;
 RT "Thymidylate synthase gene expression is stimulated by some (but not
 RT all) introns.";
 RL Nucleic Acids Res. 17:645-658(1989).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 CC -----
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 CC -----
 DR EMBL; M13019; AAA40439.1; -;
 DR EMBL; M13352; AAA40444.1; -;
 DR EMBL; J02617; AAA40444.1; JOINED.
 DR EMBL; M13347; AAA40444.1; JOINED.
 DR EMBL; M13348; AAA40444.1; JOINED.
 DR EMBL; M13349; AAA40444.1; JOINED.
 DR EMBL; M13350; AAA40444.1; JOINED.
 DR EMBL; M13351; AAA40444.1; JOINED.
 DR EMBL; X14489; CAA32851.1; -;
 DR PIR; A26323; YXMST.
 DR HSSP; P45352; LRFS.
 DR MGD; MGI:98878; Tmys.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat_synth; 1.
 DR PRINTS; PR00108; THYMSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 FT ACT SITE 189 By similarity.
 SQ SEQUENCE 307 AA; 34958 MW; E4930618C487FD5E CRC64;
 Query Match 91.2%; Score 31; DB 1; Length 307;
 Best Local Similarity 80.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CHAVC 5
 Db 189 CHALC 193
 RESULT 85
 TISY_RAT
 ID TISY_RAT STANDARD; PRT; 307 AA.
 AC P45352;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=Tmys;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95226450; PubMed=7711067; DOI=10.1016/0167-4781(95)00008-5;
 RA Ciesla J., Weiner K.X., Weiner R.S., Reeton J.T., Maley G.F.,
 RA Maley F.;
 RT "Isolation and expression of rat thymidylate synthase cDNA:
 RT phylogenetic comparison with human and mouse thymidylate synthases.";
 RL Biochim. Biophys. Acta 1261:233-242(1995).
 RP [2]
 RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
 RX MEDLINE=99110611; PubMed=9894005; DOI=10.1021/bi981881d;
 RA Sotelo-Mundo R.R., Ciesla J., Dziak J.M., Rode W., Maley F.,
 RA Maley G.F., Hardy L.W., Montfort W.R.;
 RT "Crystal structures of rat thymidylate synthase inhibited by Tomudex,
 RT a potent anticancer drug.";
 RL Biochemistry 38:1087-1094(1999).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 CC -----
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 CC -----
 DR EMBL; L12138; AAA92340.1; -;
 DR PIR; S53715; S53715.
 DR PDB; 1RTS; X-ray; A/B=1-307.
 DR PDB; 2TST; X-ray; A/B/C/D=1-307.
 DR RGD; 3921; Tmys.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW 3D-structure; Methyltransferase; Nucleotide biosynthesis; Transferase.
 FT ACT SITE 189 By similarity.
 FT TURN 23 23
 FT HELIX 24 37
 FT STRAND 39 41
 FT STRAND 49 60
 FT TURN 62 63
 FT HELIX 75 86
 FT TURN 87 88
 FT STRAND 91 91
 FT TURN 92 92
 FT HELIX 93 96
 FT TURN 97 99
 FT TURN 102 104
 FT HELIX 105 107
 FT STRAND 109 114
 FT TURN 115 116
 FT TURN 122 123
 FT STRAND 124 124
 FT HELIX 129 134
 FT STRAND 136 136
 FT TURN 137 137
 FT TURN 143 144
 FT TURN 148 149
 FT STRAND 152 152
 FT HELIX 154 164
 FT TURN 166 167
 FT STRAND 172 174
 FT TURN 178 180
 FT HELIX 181 183
 FT STRAND 190 198

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FT TURN 199 200
FT STRAND 201 212
FT TURN 213 215
FT HELIX 216 235
FT TURN 236 236
FT STRAND 238 252
FT HELIX 253 255
FT HELIX 256 264
FT STRAND 272 275
FT HELIX 282 284
FT HELIX 287 289
FT STRAND 290 293
SQ SEQUENCE 307 AA; 159F564D347B2B52 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 307;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 189 CHALC 193

RESULT 86
Q9D0H1 PRELIMINARY; PRT; 307 AA.
AC Q9D0H1 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610017621 product:thymidylate synthase, full
DE insert sequence.
DE Name=Tyms;
GS Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Tazawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -|- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -|- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; AK011435; BAB27620.1; -.
DR HSSP; P45352; 1RTS.
DR MGD; MGI:98878; Tyms.
DR GO; GO:0008168; P:methyltransferase activity; IEA.
DR GO; GO:0004799; P:thymidylate synthase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat_synth.
DR Pfam; PF00303; Thymidylat_synth; 1.
DR PRINTS; PD00108; THYMDSNTTHASE.
DR PRODOM; PD001180; Thymidylat_synth; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 34989 MW; E4930618C52CE7EE CRC64;

Query Match 91.2%; Score 31; DB 2; Length 307;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 189 CHALC 193

RESULT 87
Q8VDV6 PRELIMINARY; PRT; 307 AA.
AC Q8VDV6;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tyms protein.
GN Name=Tyms;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C2ECH II; TISSUE=Mammary tumor;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; BC020119; AAH20139.1; --
DR HSSP; P45352; IRTS.
DR MGD; MGI:98878; Tyms.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR Pfam; PF00303; Thymidylat synt; 1.
DR PRINTS; PR00108; THYMDSNTHASE.
DR PRODOM; PD001180; Thymidylat synth; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 34930 MW; 76F797162468FD9D CRC64;

Query Match 91.2%; Score 31; DB 2; Length 307;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 189 CHALC 193

RESULT 88
ID Q8MQS5 PRELIMINARY; PRT; 310 AA.
AC Q8MQS5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE GH05249p (Fragment).
GN ORFNames=CG4342;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe R., Chavez C., Dorsett V., Dreesen D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY128415; AAM75008.1; --
DR FlyBase; FBgn0038791; CG4342.
FT NON TER 1
SQ SEQUENCE 310 AA; 34213 MW; 7641F9761512F5CC CRC64;
Query Match 91.2%; Score 31; DB 2; Length 310;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 93 CHALC 97

RESULT 89
TYSY_HUMAN
ID TYSY_HUMAN STANDARD; PRT; 312 AA.
AC P04818;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (Tsase) (OK/SW-cl.29).
GN Name=TYMS; Synonyms=TS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215597; PubMed=2987839;
RA Takeichi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T.;
RT "Nucleotide sequence of a functional cDNA for human thymidylate
RT synthase.";
RL Nucleic Acids Res. 13:2035-2043 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91056070; PubMed=2243092;
RA Kaneda S., Nalbantoglu J., Takeichi K., Shimizu K., Gotoh O., Seno T.,
RA Ayusawa D.;
RT "Structural and functional analysis of the human thymidylate synthase
RT gene.";
RL J. Biol. Chem. 265:20277-20284 (1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon adenocarcinoma;
RA Shichijo S., Iton K.;
RT "Identification of immuno-peptidmics that recognized by tumor-reactive
RT CTL generated from TIL of colon cancer patients.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow, and Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-67 FROM N.A.
RX MEDLINE=90110051; PubMed=2532645;
RA Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T.;
RT "Human thymidylate synthase gene: isolation of phage clones which
RT cover a functionally active gene and structural analysis of the region
RT upstream from the translation initiation codon.";
RL J. Biochem. 106:575-583(1989).
RN [6]
RP SEQUENCE OF 1-24.
RX MEDLINE=85261174; PubMed=3839505;
RA Shimizu K., Ayusawa D., Takeishi K., Seno T.;
RT "Purification and NH2-terminal amino acid sequence of human
RT thymidylate synthase in an overproducing transformant of mouse FM3A
RT cells.";
RL J. Biochem. 97:845-850(1985).
RN [7]
RP SEQUENCE OF 1-9.
RX PubMed=2656695;
RA Davison V.J., Sirawaraporn W., Santi D.V.;
RT "Expression of human thymidylate synthase in *Escherichia coli*.";
RL J. Biol. Chem. 264:9145-9148(1989).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=96110704; PubMed=8845352;
RA Schiffer C.A., Clifton I.J., Davison V.J., Santi D.V., Stroud R.M.;
RT "Crystal structure of human thymidylate synthase: a structural
RT mechanism for guiding substrates into the active site.";
RL Biochemistry 34:16279-16287(1995).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=21229106; PubMed=11329255; DOI=10.1021/bi002413i;
RA Phan J., Koli S., Minor W., Dunlap R.B., Berger S.H., Lebioda L.;
RT "Human thymidylate synthase is in the closed conformation when
RT complexed with dUMP and raltitrexed, an antifolate drug.";
RL Biochemistry 40:1897-1902(2001).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21216721; PubMed=11278511; DOI=10.1074/jbc.M009493200;
RA Phan J., Steadman D.J., Koli S., Ding W.C., Minor W., Dunlap R.B.,
RA Berger S.H., Lebioda L.;
RT "Structure of human thymidylate synthase suggests advantages of
RT chemotherapy with noncompetitive inhibitors.";
RL J. Biol. Chem. 276:14170-14177(2001).
CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -I- SUBUNIT: Homodimer.
CC -I- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X02308; CAA26178.1; -;
DR EMBL: D00596; BAA00472.1; -;
DR EMBL: A8062290; BAB93473.1; -;
DR EMBL: BC002567; AAO02567.1; -;
DR EMBL: BC013919; AAI13919.1; -;
DR EMBL: D00517; BAA00404.1; -;
DR PIR: A23047; YXHUT.
DR PDB: 1HWY; X-ray; A/B/C/D=25-312.
DR PDB: 1HW3; X-ray; A=1-312.
DR PDB: 1HW4; X-ray; A=1-312.
DR PDB: 1HW2; X-ray; A/B=23-312.
DR PDB: 1I00; X-ray; A/B=23-312.
DR PDB: 1JU6; X-ray; A/B/C/D=1-312.

DR PDB: 1JUJ; X-ray; A/B/C/D=1-312.
DR Genew: HGNC:12441; TVMS.
DR H-InvDB: HIX0017793; -;
DR Reactome: P04818; -;
DR MIM: 188350; -;
DR GO: GO:0009157; P:deoxyribonucleoside monophosphate biosynthesis; TAS.
DR GO: GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . .; TAS.
DR InterPro: IPR000398; Thymidylat synth.
DR Pfam: PF00303; Thymidylat synt; 1.
DR PRINTS: PRO0108; THYMDSNTASE.
DR ProDom: PD001180; Thymidylat synth; 1.
DR PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.
KW 3D-structure; Direct protein sequencing; Methyltransferase;
KW Nucleotide biosynthesis; Transferase.
FT INIT MET 0
FT ACT_SITE 194 194
FT TURN 28 28
FT HELIX 29 42
FT STRAND 44 46
FT TURN 49 50
FT STRAND 54 65
FT TURN 67 68
FT TURN 74 77
FT HELIX 80 91
FT TURN 92 93
FT STRAND 96 96
FT HELIX 97 101
FT TURN 102 104
FT TURN 107 109
FT HELIX 110 112
FT HELIX 114 119
FT TURN 120 121
FT TURN 123 124
FT STRAND 127 128
FT STRAND 129 129
FT HELIX 134 140
FT STRAND 141 141
FT TURN 142 142
FT TURN 148 149
FT TURN 153 154
FT STRAND 157 157
FT HELIX 159 169
FT TURN 171 172
FT TURN 174 175
FT STRAND 177 179
FT TURN 183 185
FT HELIX 186 188
FT STRAND 195 203
FT TURN 204 205
FT STRAND 206 217
FT TURN 218 220
FT HELIX 221 239
FT STRAND 240 241
FT STRAND 243 257
FT HELIX 258 260
FT HELIX 261 268
FT TURN 269 269
FT STRAND 277 280
FT HELIX 287 289
FT HELIX 292 294
FT STRAND 295 298
SQ SEQUENCE 312 AA; 35584 MW; A66F056D1973AB41 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 312;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
DB 194 CHALC 198

RESULT 90

Q6P045 Q6P045 PRELIMINARY; PRT; 318 AA.
 ID Q6P045;
 DT 05-JUN-2004 (TrEMBLrel. 27, Created)
 DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
 DE Zgc:56465 protein.
 GN Name=zgc:56465; ORFNames=zgc:77659;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX Strausberg R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; BC065845; AAH65845.1; -;
 DR ZFIN; ZDB-GENE-040426-60; zgc:77659.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat_synth.
 DR PRINTS; PR00108; THYMDNSTHASE.
 DR PRODOM; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 318 AA; 36183 MW; 47E9BABA24927372 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 318;
 Best Local Similarity 80.0%; Pred. No. 6.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 200 CHALC 204
 RESULT 91
 Q7ZUI7 PRELIMINARY; PRT; 319 AA.
 ID Q7ZUI7

Q7ZUI7;
 01-JUN-2003 (TrEMBLrel. 24, Created)
 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tyms protein.
 GN ORFNames=zgc:56465;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole body;
 RX Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; BC049026; AAH49026.1; -;
 DR HSSP; P04818; 1HW4.
 DR ZFIN; ZDB-GENE-040426-59; zgc:56465.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat_synth.
 DR Pfam; PF00303; thymidylat_synth; 1.
 DR PRINTS; PR00108; THYMDNSTHASE.
 DR PRODOM; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 319 AA; 36299 MW; ADF451E1DDF891A CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 319;
 Best Local Similarity 80.0%; Pred. No. 6.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHAVC 5
 DB 201 CHALC 205
 RESULT 92
 Q9DGH5 PRELIMINARY; PRT; 319 AA.
 ID Q9DGH5
 AC Q9DGH5;

DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Thymidylate synthase.
 GN ORFNames=zgc:56465;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gill R.L. Jr., Warren J.T. Jr.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; AY005804; AAF97476.1; -.
 DR HSSP; P04818; 1HW4.
 DR ZFIN; ZDB-GENE-040426-59; ZGC:56465.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat_synth.
 DR Pfam; PF00303; Thymidylat_synth.
 DR PRINTS; PR00108; THYMDNSTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide_biosynthesis; Transferase.
 SQ SEQUENCE 319 AA; 36313 MW; E08B155B09DE1E84 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 319;
 Best Local Similarity 80.0%; Pred. No. 6.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 DB 201 CHALC 205

RESULT 93
 ID P91501 PRELIMINARY; PRT; 373 AA.
 AC P91501;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein T27A3.7;
 GN Names=T27A3.7; ORFNames=T27A3.7;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RX MEDLINE=99069613; PubMed=9851916;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Murray J., Wohldmann P.;
 RT "The sequence of C. elegans cosmid T27A3.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;

RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88180; AAB42300.1; -.
 DR PIR; T25920; T25920.
 DR WormBase; WBGene0020843; T27A3.7.
 DR WormPep; T27A3.7; CE14229.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR00345; CYC heme BS.
 DR InterPro; IPR002219; DAG PE-bind.
 DR InterPro; IPR011011; FYVE_PHD_ZnF.
 DR SMART; SM00109; C1; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 373 AA; 42560 MW; F5DDFEFC9FCF29B9 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 373;
 Best Local Similarity 80.0%; Pred. No. 7.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
 DB 262 CHALC 266

RESULT 94
 ID Q8EED1 PRELIMINARY; PRT; 380 AA.
 AC Q8EED1;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Hypothetical protein SO2451.
 GN OrderedLocusNames=SO2451;
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Shewanellaceae; Shewanella.
 OX NCBI_TaxID=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MR-1;
 RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.B., Methe B.A.,
 RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
 RA Brinkak L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imbraim M.,
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
 RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
 RA Venter J.C., Nealeson K.H., Fraser C.M.;
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis.";
 RL Nat. Biotechnol. 20:1118-1123 (2002).
 DR EMBL; AE015686; AAN55485.1; -.
 DR TIGR; SO2451; -.
 KW Complete proteome.
 SQ SEQUENCE 380 AA; 42539 MW; 562E0C3E60B5CF0F CRC64;

Query Match 91.2%; Score 31; DB 2; Length 380;
 Best Local Similarity 80.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

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Query Match      91.2%; Score 31; DB 2; Length 391;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 21 CHSVC 25
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PRELIMINARY; PRT; 387 AA.
Q8XR48
AC Q8XR48;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PUTATIVE TRANSFERASE PROTEIN (EC 2.-.-.-).
GN Name=RS02347; OrderedLocNames=RS1013;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaepin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646082; CAD18164.1; -
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
KW Complete proteome; Plasmid; Transferase.
SQ SEQUENCE 387 AA; 43792 MW; AC2519AF673BE64D9 CRC64;

Query Match      91.2%; Score 31; DB 2; Length 387;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 271 CHAMC 275
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1 CHAVC 5
PRELIMINARY; PRT; 391 AA.
Q756Y7
AC Q756Y7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AER127Cp.
GN ORFNames=AER127C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Gates K., Dietrich F.S., Brachat S., Voegeli S.E., Lerch A.,
RA Philippsen P., Giffney T.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016818; AAS52810.1; -
DR AGD; AER137C; -
DR GO; GO:006284; P:base-excision repair; IEA.
DR InterPro; IPR011257; DNA glycosylase.
DR InterPro; IPR003265; Endo_3c.
DR Pfam; PF00730; HHX-GPD; 1.
DR SMART; SM00478; ENDO3c; 1.
SQ SEQUENCE 391 AA; 44532 MW; 518E109A6FD64780 CRC64;

Query Match      91.2%; Score 31; DB 2; Length 404;
Best Local Similarity 80.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 142 CHALC 146
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1 CHAVC 5
PRELIMINARY; PRT; 404 AA.
Q6DD56
AC Q6DD56;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Alg2-prov protein.
GN Name=alg2-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077444; AAH77444.1; -
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco trans 1.
DR Pfam; PF00534; Glycos transf 1; 1.
SQ SEQUENCE 404 AA; 46374 MW; 69E16E0E62559DBB CRC64;

Query Match      91.2%; Score 31; DB 2; Length 404;
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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 73 CHALC 77

RESULT 98
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DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Related to 60S ribosomal protein L2 (Mitochondrial).
GN Name=SE6.150;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AL670004; CAD21256.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR Pfam; PF01016; Ribosomal L27; 1.
DR PRINTS; PR00063; RIBOSOMAL27.
DR ProDom; PD003114; Ribosomal_L27; 1.
DR Ribosomal protein.
SQ SEQUENCE 447 AA; 49442 MW; 404A02A606F613D4 CRC64;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 18 CHSVC 22

RESULT 99
Q89GP2 PRELIMINARY; PRT; 481 AA.
AC Q89GP2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE B116303 protein.
GN OrderedLocustNames=b116303;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110.
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Teurtocka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005958; BAC51568.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; Polysacc_synt.
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DR Pfam; PF01943; Polysacc_synt; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 52048 MW; CAD37FB12B1B34D8 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 481;
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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 389 CHALC 393

RESULT 100
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AC Q7QDE4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCF10190.
GN Name=agCG47224; ORFNames=ENSANGG00000011737;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA80100851; EAA07305.1; -.
SQ SEQUENCE 502 AA; 55977 MW; 89AC334BCE3B2E8C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 502;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 276 CHALC 280

Search completed: July 27, 2005, 00:01:04
Job time : 178 secs
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: July 27, 2005, 00:01:11 ; Search time 157 Seconds
(without alignments)
12.388 Million cell updates/sec

Title: US-10-632-678-10

Perfect score: 34

Sequence: 1 CHAVC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 38892284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	34	100.0	5	US-10-006-982-8
5	34	100.0	5	US-10-105-008-96
6	34	100.0	5	US-10-058-821-10
7	34	100.0	5	US-10-359-546-10
8	34	100.0	5	US-10-369-226-22
9	34	100.0	5	US-10-369-226-34
10	34	100.0	5	US-10-425-557-10
11	34	100.0	5	US-10-412-701-10
12	34	100.0	5	US-10-632-678-10
13	34	100.0	5	US-10-759-379-296
14	34	100.0	5	US-10-759-507-296
15	34	100.0	5	US-10-836-289-20
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Sequence 151715,
Sequence 197235,
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Sequence 191667,
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Sequence 167243,
Sequence 233727,
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Sequence 233725,
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87 33 97.1 913 16 US-10-437-963-197899 Sequence 197899,
88 33 97.1 946 16 US-10-437-963-188555 Sequence 188555,
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90 31 91.2 18 16 US-10-629-313-150 Sequence 150, App
91 31 91.2 20 9 US-09-864-761-35523 Sequence 35523, A
92 31 91.2 49 16 US-10-437-963-174571 Sequence 174571,
93 31 91.2 51 16 US-10-425-115-211467 Sequence 211467,
94 31 91.2 55 15 US-10-424-599-163830 Sequence 163830,
95 31 91.2 63 9 US-09-864-761-34873 Sequence 34873, A
96 31 91.2 67 15 US-10-424-599-190876 Sequence 190876,
97 31 91.2 96 15 US-10-291-265-762 Sequence 762, App
98 31 91.2 96 16 US-10-425-115-201825 Sequence 201825,
99 31 91.2 98 16 US-10-437-963-118366 Sequence 118366,
100 31 91.2 100 15 US-10-424-599-183087 Sequence 183087,

ALIGNMENTS

RESULT 1
US-09-234-395-296
; Sequence 296, Application US/09234395
; Patent No. US2002012304A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C2
; CURRENT APPLICATION NUMBER: US/09/234,395
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-296

Query Match 100.0%; Score 34; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5
RESULT 2
US-09-305-928-296
; Sequence 296, Application US/09305928
; Patent No. US20020146687A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C4
; CURRENT APPLICATION NUMBER: US/09/305,928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-296

Query Match 100.0%; Score 34; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 3
US-09-769-145-10
; Sequence 10, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-10

Query Match 100.0%; Score 34; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5
RESULT 4
US-10-006-982-8
; Sequence 8, Application US/10006982
; Publication No. US20020151475A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED IP LAW GROUP PLLC

STREET: 6300 Bank of America Bldg., 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/006,982

FILING DATE: 04-Dec-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 100086.401C11

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: circular

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-006-982-8

Query Match 100.0%; Score 34; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 5

US-10-105-008-96

Sequence 96, Application US/10105008

Publication No. US20030065136A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

APPLICANT: Farookhi, Riaz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

FILE REFERENCE: 100086.401D1

CURRENT APPLICATION NUMBER: US/10/105,008

CURRENT FILING DATE: 2002-03-22

NUMBER OF SEQ ID NOS: 99

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 96

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-10-105-008-96

Query Match 100.0%; Score 34; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

Db 1 CHAVC 5

RESULT 6

US-10-058-821-10

Sequence 10, Application US/10058821

Publication No. US20030087811A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

APPLICANT: Farookhi, Riaz

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CANCER THERAPY

FILE REFERENCE: 100086.401C12

CURRENT APPLICATION NUMBER: US/10/058,821

CURRENT FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-10-058-821-10

Query Match 100.0%; Score 34; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

RESULT 7

US-10-359-546-10

Sequence 10, Application US/10359546

Publication No. US20030224978A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING APOPTOSIS

FILE REFERENCE: 100086.401C15

CURRENT APPLICATION NUMBER: US/10/359,546

CURRENT FILING DATE: 2003-02-04

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 5

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

OTHER INFORMATION: and/or C-terminal modifications such as amide or

OTHER INFORMATION: ester group

US-10-359-546-10

Query Match 100.0%; Score 34; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db 1 CHAVC 5

```
Db          1 CHAVC 5

RESULT 8
US-10-369-226-22
; Sequence 22, Application US/10369226
; Publication No. US20030236186A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
; INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/369,226
; FILING DATE: 13-Feb-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 100086.406C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-369-226-22

Query Match          100.0%; Score 34; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CHAVC 5
           |||||
Db          1 CHAVC 5

RESULT 9
US-10-369-226-34
; Sequence 34, Application US/10369226
; Publication No. US20030236186A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
; INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

US-10-369-226-34

Query Match          100.0%; Score 34; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CHAVC 5
           |||||
Db          1 CHAVC 5

RESULT 10
US-10-425-557-10
; Sequence 10, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zenjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425.557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-10

Query Match          100.0%; Score 34; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CHAVC 5
           |||||
Db          1 CHAVC 5
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RESULT 11
US-10-412-701-10
; Sequence 10, Application US/10412701
; Publication No. US2004005864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-10
Query Match 100.0%; Score 34; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT 12
US-10-632-678-10
; Sequence 10, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farooqui, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-10
Query Match 100.0%; Score 34; DB 16; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT 13
US-10-759-379-296
; Sequence 296, Application US/10759379
; Publication No. US20040248219A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C12
; CURRENT APPLICATION NUMBER: US/10/759,379
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 09/305,928
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 09/234,395
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 09/187,859
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/073,040
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-10-759-379-296
Query Match 100.0%; Score 34; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHAVC 5
Db 1 CHAVC 5
RESULT 14
US-10-759-507-296
; Sequence 296, Application US/10759507
; Publication No. US20040248220A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C11
; CURRENT APPLICATION NUMBER: US/10/759,507
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 09/234,395
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 09/187,859
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/073,040
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: N-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-10-759-507-296

Query Match 100.0%; Score 34; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 15

US-10-836-289-20
; Sequence 20, Application US/10836289
; Publication No. US2005004013A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: FRIEDLANDER, Martin
; APPLICANT: DORRELL, Michael. I.
; TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: TSRI-987.1
; CURRENT APPLICATION NUMBER: US/10/836,289
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/467,188
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CYCLIC CADHERIN ANTAGONIST, DISULFIDE BOND BETWEEN
; OTHER INFORMATION: Cys1 and Cys5
US-10-836-289-20

Query Match 100.0%; Score 34; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 16

US-09-769-145-81
; Sequence 81, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-81

Query Match 100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 17

US-09-769-145-84
; Sequence 84, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-84

Query Match 100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 1 CHAVC 5

RESULT 18

US-09-769-145-85
; Sequence 85, Application US/09769145
; Patent No. US20020168761A1

GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 10086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-85

Query Match 100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 2 CHAVC 6

RESULT 19
US-09-769-145-88
; Sequence 88, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 10086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-88

Query Match 100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 20
US-09-769-145-89
; Sequence 89, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 10086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-89

Query Match 100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 21
US-09-769-145-90
; Sequence 90, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 10086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 90
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-09-769-145-90

Query Match 100.0%; Score 34; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||||
Db 1 CHAVC 5

RESULT 22

US-10-105-008-10
; Sequence 10, Application US/10105008
; Publication No. US20030065136A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401D1
; CURRENT APPLICATION NUMBER: US/10/105,008
; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-105-008-10

Query Match 100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||||
Db 2 CHAVC 6

RESULT 23

US-10-105-008-84
; Sequence 84, Application US/10105008
; Publication No. US20030065136A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401D1
; CURRENT APPLICATION NUMBER: US/10/105,008
; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-105-008-84

Query Match 100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||||
Db 1 CHAVC 5

RESULT 24

US-10-105-008-87
; Sequence 87, Application US/10105008
; Publication No. US20030065136A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401D1
; CURRENT APPLICATION NUMBER: US/10/105,008
; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-105-008-87

Query Match 100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||||
Db 1 CHAVC 5

RESULT 25

US-10-105-008-88
; Sequence 88, Application US/10105008
; Publication No. US20030065136A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401D1
; CURRENT APPLICATION NUMBER: US/10/105,008
; CURRENT FILING DATE: 2002-03-22

; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-105-008-88

Query Match 100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
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|
|
Db 2 CHAVC 6

RESULT 26

US-10-105-008-91

; Sequence 91, Application US/10105008
; Publication No. US20030065136A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Gour, Barbara J.

; APPLICANT: Farookhi, Riaz

; APPLICANT: Ali, Ammar

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

; FILE REFERENCE: 100086.401D1

; CURRENT APPLICATION NUMBER: US/10/105.008

; CURRENT FILING DATE: 2002-03-22

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 91

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

; OTHER INFORMATION: and/or C-terminal modifications such as amide or

; OTHER INFORMATION: ester group

US-10-105-008-91

Query Match 100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
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|
|
Db 1 CHAVC 5

RESULT 27

US-10-105-008-92

; Sequence 92, Application US/10105008

; Publication No. US20030065136A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Gour, Barbara J.

; APPLICANT: Farookhi, Riaz

; APPLICANT: Ali, Ammar

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

; FILE REFERENCE: 100086.401D1

; CURRENT APPLICATION NUMBER: US/10/105.008

; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or

; OTHER INFORMATION: ester group

US-10-105-008-92

Query Match 100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
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|
|
Db 1 CHAVC 5

RESULT 28

US-10-105-008-93

; Sequence 93, Application US/10105008

; Publication No. US20030065136A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Gour, Barbara J.

; APPLICANT: Farookhi, Riaz

; APPLICANT: Ali, Ammar

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

; FILE REFERENCE: 100086.401D1

; CURRENT APPLICATION NUMBER: US/10/105.008

; CURRENT FILING DATE: 2002-03-22

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 93

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide

; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence

; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal

; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group

; OTHER INFORMATION: and/or C-terminal modifications such as amide or

; OTHER INFORMATION: ester group

US-10-105-008-93

Query Match 100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|
|
|
|
|
Db 1 CHAVC 5

RESULT 29

US-10-105-008-95

; Sequence 95, Application US/10105008

; Publication No. US20030065136A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Gour, Barbara J.

; APPLICANT: Farookhi, Riaz

; APPLICANT: Ali, Ammar

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

; FILE REFERENCE: 100086.401D1

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; CURRENT APPLICATION NUMBER: US/10/105,008
; CURRENT FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-105-008-95

Query Match          100.0%; Score 34; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||||
Db 1 CHAVC 5

RESULT 30
US-10-425-557-81
; Sequence 81, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zhenjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425,557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-81

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||||
Db 1 CHAVC 5

RESULT 31
US-10-425-557-84
; Sequence 84, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zhenjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425,557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-84

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||||
Db 1 CHAVC 5

RESULT 32
US-10-425-557-85
; Sequence 85, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Ammar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zhenjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425,557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-85

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-89

Query Match      100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      1 CHAVC 5

RESULT 35
US-10-425-557-90
; Sequence 90, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425.557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-90

Query Match      100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      1 CHAVC 5

RESULT 36
US-10-412-701-81
; Sequence 81, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; FEATURE:
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-89

Query Match      100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      1 CHAVC 5

RESULT 34
US-10-425-557-89
; Sequence 89, Application US/10425557
; Publication No. US20040006011A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shaomeng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.401C16
; CURRENT APPLICATION NUMBER: US/10/425.557
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
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```
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-81

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      1 CHAVC 5

RESULT 37
US-10-412-701-84
; Sequence 84, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-84

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      1 CHAVC 5

RESULT 38
US-10-412-701-85
; Sequence 85, Application US/10412701
```

```
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-85

Query Match          100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
        |||||
Db      2 CHAVC 6

RESULT 39
US-10-412-701-88
; Sequence 88, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-88

Query Match          100.0%; Score 34; DB 15; Length 6;
```

Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 CHAVC 5
 |||||
Db 1 CHAVC 5

RESULT 40

US-10-412-701-89
; Sequence 89, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89

LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-89

Query Match 100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
Db 1 CHAVC 5

RESULT 41

US-10-412-701-90
; Sequence 90, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90

LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-90

Query Match 100.0%; Score 34; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
Db 1 CHAVC 5

RESULT 42

US-10-632-678-84
; Sequence 84, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84

LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-84

Query Match 100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
 |||||
Db 1 CHAVC 5

RESULT 43

US-10-632-678-87
; Sequence 87, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-87

Query Match 100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
| | | | |
Db 1 CHAVC 5

RESULT 44

US-10-632-678-88
; Sequence 88, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-88

Query Match 100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
| | | | |
Db 2 CHAVC 6

RESULT 45

US-10-632-678-91
; Sequence 91, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01

; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-91

Query Match 100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
| | | | |
Db 1 CHAVC 5

RESULT 46

US-10-632-678-92
; Sequence 92, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-92

Query Match 100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
| | | | |
Db 1 CHAVC 5

RESULT 47

US-10-632-678-93
; Sequence 93, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION

```
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632.678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-10-632-678-93

Query Match      100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 48
US-10-632-678-100
; Sequence 100, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Farcokhi, Riaz
; APPLICANT: Ali, Anmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632.678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-10-632-678-100

Query Match      100.0%; Score 34; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||||
Db      2 CHAVC 6

RESULT 49
US-09-769-145-86
; Sequence 86, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
```

```
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-09-769-145-86

Query Match      100.0%; Score 34; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
      |||||
Db      1 CHAVC 5

RESULT 50
US-09-769-145-87
; Sequence 87, Application US/09769145
; Patent No. US20020168761A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Anmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 100086.413C1
; CURRENT APPLICATION NUMBER: US/09/769,145
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 09/491,078
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; US-09-769-145-87

Query Match      100.0%; Score 34; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-425-557-87

Query Match 100.0%; Score 34; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 2 CHAVC 6

RESULT 55

US-10-412-701-86
; Sequence 86, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Annmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian
; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 10086 413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-86

Query Match 100.0%; Score 34; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 56

US-10-412-701-87
; Sequence 87, Application US/10412701
; Publication No. US20040058864A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Ali, Annmar
; APPLICANT: Ni, Feng
; APPLICANT: Chen, Zhigang
; APPLICANT: Michaud, Stephanie Denise
; APPLICANT: Wang, Shoameng
; APPLICANT: Hu, Zengjian

; TITLE OF INVENTION: PEPTIDOMIMETIC MODULATORS OF CELL ADHESION
; FILE REFERENCE: 10086.413C2
; CURRENT APPLICATION NUMBER: US/10/412,701
; CURRENT FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-412-701-87

Query Match 100.0%; Score 34; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 2 CHAVC 6

RESULT 57

US-10-632-678-89
; Sequence 89, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annmar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 10086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-89

Query Match 100.0%; Score 34; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 1 CHAVC 5

RESULT 58

US-10-632-678-90
; Sequence 90, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-90

Query Match 100.0%; Score 34; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
| | | | |
Db 2 CHAVC 6

RESULT 59

US-10-632-678-96
; Sequence 96, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-96

Query Match 100.0%; Score 34; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
| | | | |
Db 3 CHAVC 7

RESULT 60

US-10-632-678-95
; Sequence 95, Application US/10632678

; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
US-10-632-678-95

Query Match 100.0%; Score 34; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
| | | | |
Db 3 CHAVC 7

RESULT 61

US-10-632-678-101
; Sequence 101, Application US/10632678
; Publication No. US20040106545A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; APPLICANT: Farookhi, Riaz
; APPLICANT: Ali, Annar
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELL ADHESION
; FILE REFERENCE: 100086.401C18
; CURRENT APPLICATION NUMBER: US/10/632,678
; CURRENT FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic Peptide
; OTHER INFORMATION: with Classical Cell Adhesion Recognition Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide may comprise N-terminal
; OTHER INFORMATION: modification such as acetyl or alkoxybenzyl group
; OTHER INFORMATION: and/or C-terminal modifications such as amide or
; OTHER INFORMATION: ester group
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Where Xaa is beta,beta-dimethyl cysteine
US-10-632-678-101

Query Match 100.0%; Score 34; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5

Db |||||
3 CHAVC 7

RESULT 62

US-10-424-599-172220
; Sequence 172220, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 172220
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_126531C.1.pep
US-10-424-599-172220

Query Match 100.0%; Score 34; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db |||||
30 CHAVC 34

RESULT 63

US-10-437-963-133433
; Sequence 133433, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133433
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35303C.1.pep
US-10-437-963-133433

Query Match 100.0%; Score 34; DB 16; Length 62;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db |||||
42 CHAVC 46

RESULT 64

US-10-221-278-630

; Sequence 630, Application US/10221278

; Publication No. US20040034208A1

US-10-425-115-323830
; Sequence 323830, Application US/10425115
; Publication No. US20040214272A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 323830
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_58402C.1.pep
US-10-425-115-323830

Query Match 100.0%; Score 34; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db |||||
23 CHAVC 27

RESULT 65

US-10-291-172-630
; Sequence 630, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 630
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-630

Query Match 100.0%; Score 34; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db |||||
61 CHAVC 65

RESULT 66

US-10-221-278-630

; Sequence 630, Application US/10221278

; Publication No. US20040034208A1

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; PRIOR FILING DATE: 2002-09-06
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 630
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-630

Query Match 100.0%; Score 34; DB 15; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 61 CHAVC 65

RESULT 67

US-10-437-963-196854
; Sequence 196854, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 196854
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92667C.1.pep
US-10-437-963-196854

Query Match 100.0%; Score 34; DB 16; Length 210;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 113 CHAVC 117

RESULT 68

US-10-003-806-8
; Sequence 8, Application US/10003806

; Publication No. US20020119929A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Colin E.
; APPLICANT: Agoulnik, Alexander I.
; APPLICANT: Zhu, Qichao
; TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
; FILE REFERENCE: P02066US1/10024824
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-003-806-8

Query Match 100.0%; Score 34; DB 13; Length 380;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 318 CHAVC 322

RESULT 69

US-10-437-963-137415
; Sequence 137415, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 137415
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38900C.1.pep
US-10-437-963-137415

Query Match 100.0%; Score 34; DB 16; Length 382;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 36 CHAVC 40

RESULT 70

US-10-437-963-151715
; Sequence 151715, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 151715
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51834C.1.pep
US-10-437-963-151715

Query Match 100.0%; Score 34; DB 16; Length 424;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 39 CHAVC 43

RESULT 71
US-10-437-963-197235
; Sequence 197235, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197235
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93010C.1.pep
US-10-437-963-197235

Query Match 100.0%; Score 34; DB 16; Length 513;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 190 CHAVC 194

RESULT 72
US-10-047-542-74
; Sequence 74, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.C1P1

; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-047-542-74

Query Match 100.0%; Score 34; DB 13; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 96 CHAVC 100

RESULT 73
US-10-425-115-315958
; Sequence 315958, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 315958
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_51224C.1.pep
US-10-425-115-315958

Query Match 97.1%; Score 33; DB 16; Length 76;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 55 CHAVC 59

RESULT 74
US-10-425-115-191667
; Sequence 191667, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 191667
; LENGTH: 82
; TYPE: PRT

; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106382C.1.pep
US-10-425-115-191667

Query Match 97.1%; Score 33; DB 16; Length 82;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 50 CHAIC 54

RESULT 75

US-10-437-963-159565
; Sequence 159565, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 159565
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5892C.1.pep
US-10-437-963-159565

Query Match 97.1%; Score 33; DB 16; Length 102;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 48 CHAIC 52

RESULT 76

US-10-424-599-167243
; Sequence 167243, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167243
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(110)
; OTHER INFORMATION: unsure at all xaa locations

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_122038C.1.pep
US-10-424-599-167243

Query Match 97.1%; Score 33; DB 15; Length 110;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 83 CHAIC 87

RESULT 77

US-10-424-599-233727
; Sequence 233727, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233727
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53080C.1.pep
US-10-424-599-233727

Query Match 97.1%; Score 33; DB 15; Length 241;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
Db 104 CHAIC 108

RESULT 78

US-10-424-599-276468
; Sequence 276468, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276468
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91670C.1.pep
US-10-424-599-276468

Query Match 97.1%; Score 33; DB 15; Length 242;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5

Db 104 CHAIC 108
|||:|

RESULT 79

US-10-424-599-233725
; Sequence 233725, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233725
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53079C.1.pep
US-10-424-599-233725

Query Match 97.1%; Score 33; DB 15; Length 243;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 106 CHAIC 110

RESULT 80

US-10-437-963-178188
; Sequence 178188, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178188
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_75769C.1.pep
US-10-437-963-178188

Query Match 97.1%; Score 33; DB 16; Length 280;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 217 CHAIC 221

RESULT 81

US-10-425-114-71839

; Sequence 71839, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53213)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71839
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73165F09_FLI.pep
US-10-425-114-71839

Query Match 97.1%; Score 33; DB 15; Length 314;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 309 CHAIC 313

RESULT 82

US-10-437-963-190970
; Sequence 190970, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190970
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87333C.1.pep
US-10-437-963-190970

Query Match 97.1%; Score 33; DB 16; Length 343;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 126 CHAIC 130

RESULT 83

US-10-437-963-190972
; Sequence 190972, Application US/10437963
; Publication No. US20040123343A1

GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190972
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87335C.1.pep
US-10-437-963-190972

Query Match 97.1%; Score 33; DB 16; Length 426;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 184 CHAIC 188

RESULT 84

US-10-437-963-122755
; Sequence 122755, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122755
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(728)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25654C.1.pep
US-10-437-963-122755

Query Match 97.1%; Score 33; DB 16; Length 728;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 310 CHAIC 314

RESULT 85

US-10-437-963-169219
; Sequence 169219, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169219
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6765C.1.pep
US-10-437-963-169219

Query Match 97.1%; Score 33; DB 16; Length 777;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 590 CHAIC 594

RESULT 86

US-10-437-963-201319
; Sequence 201319, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201319
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96706C.1.pep
US-10-437-963-201319

Query Match 97.1%; Score 33; DB 16; Length 892;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
|||:|
Db 657 CHAIC 661

RESULT 87

US-10-437-963-197899

; Sequence 197899, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197899
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93612C.1.pep
; US-10-437-963-197899

Query Match 97.1%; Score 33; DB 16; Length 913;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 682 CHAIC 686

RESULT 88

US-10-437-963-188555
; Sequence 188555, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 188555
; LENGTH: 946
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85148C.1.pep
; US-10-437-963-188555

Query Match 97.1%; Score 33; DB 16; Length 946;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 686 CHAIC 690

RESULT 89

US-10-629-313-146
; Sequence 146, Application US/10629313

; Publication No. US20040176572A1
; GENERAL INFORMATION:
; APPLICANT: Nelson B. Freimer
; APPLICANT: Hong Chen
; APPLICANT: Victor I. Reus
; APPLICANT: Susan K. Service
; APPLICANT: Lynne Alison McInnes
; APPLICANT: Pedro Leon
; APPLICANT: Lodewijk Sandkuijl
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18
; TITLE OF INVENTION: Related Disorders
; FILE REFERENCE: UCAL-154CIP5
; CURRENT APPLICATION NUMBER: US/10/629,313
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,544
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/631,275
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-629-313-146

Query Match 91.2%; Score 31; DB 16; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
|||:|
Db 9 CHAIC 13

RESULT 90

US-10-629-313-150
; Sequence 150, Application US/10629313
; Publication No. US20040176572A1
; GENERAL INFORMATION:
; APPLICANT: Nelson B. Freimer
; APPLICANT: Hong Chen
; APPLICANT: Victor I. Reus
; APPLICANT: Susan K. Service
; APPLICANT: Lynne Alison McInnes
; APPLICANT: Pedro Leon
; APPLICANT: Lodewijk Sandkuijl
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18
; TITLE OF INVENTION: Related Disorders
; FILE REFERENCE: UCAL-154CIP5
; CURRENT APPLICATION NUMBER: US/10/629,313
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,544
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/631,275
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 60/088,312

```
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-313-150

Query Match          91.2%; Score 31; DB 16; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||:|
Db 9 CHALC 13

RESULT 91
US-09-864-761-35523
; Sequence 35523, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35523
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```
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000512.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EST_HUMAN HIT: AI281313.1, EVALUATE 5.00e-06
US-09-864-761-35523

Query Match          91.2%; Score 31; DB 9; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||:|
Db 1 CHALC 5

RESULT 92
US-10-437-963-174571
; Sequence 174571, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174571
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72499C.1.pap
US-10-437-963-174571

Query Match          91.2%; Score 31; DB 16; Length 49;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHAVC 5
   |||:|
Db 21 CHSVC 25

RESULT 93
US-10-425-115-211467
; Sequence 211467, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```



```
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 211467
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124455C.1.pep
US-10-425-115-211467

Query Match          91.2%; Score 31; DB 16; Length 51;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 12 CHSVC 16

RESULT 94
US-10-424-599-163830
; Sequence 163830, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 163830
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118958C.1.pep
US-10-424-599-163830

Query Match          91.2%; Score 31; DB 15; Length 55;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 50 CHALC 54

RESULT 95
US-09-864-761-34873
; Sequence 34873, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34873
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007695.12
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 21
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.4
; OTHER INFORMATION: SWISSPROT HIT: P34826, EVALUATE 9.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BE729465.1, EVALUATE 4.00e-23
US-09-864-761-34873

Query Match          91.2%; Score 31; DB 9; Length 63;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHAVC 5
Db 36 CHALC 40

RESULT 96
US-10-424-599-190876
; Sequence 190876, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190876
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_115648C.1.pep
US-10-425-115-201825

Query Match          91.2%; Score 31; DB 16; Length 96;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      14 CHSVC 18

RESULT 99
US-10-437-963-118366
; Sequence 118366, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118366
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21685C.1.pep
US-10-437-963-118366

Query Match          91.2%; Score 31; DB 16; Length 98;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      75 CHAMC 79

RESULT 100
US-10-424-599-183087
; Sequence 183087, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 183087
; LENGTH: 100

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190876
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14380C.1.pep
US-10-424-599-190876

Query Match          91.2%; Score 31; DB 15; Length 67;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      52 CHSVC 56

RESULT 97
US-10-291-265-762
; Sequence 762, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-01-25
; PRIOR FILING DATE: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 762
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-762

Query Match          91.2%; Score 31; DB 15; Length 96;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHAVC 5
Db      81 CHSVC 85

RESULT 98
US-10-425-115-201825
; Sequence 201825, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201825
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136340C.1.pep
US-10-424-599-183087

Query Match      91.2%; Score 31; DB 15; Length 100;
Best Local Similarity 80.0%; Pred. NO. 8.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CHAVC 5
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Db      96 CHSVC 100
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Search completed: July 27, 2005, 00:14:44
Job time : 159 secs

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